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OM protein - protein search, using sw model

Run on: December 10, 2002, 09:57:25 : Search time 12 Seconds
(without alignments)
610.440 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318

Sequence: 1 MESSPPIQSSGNSSTLGRVP.....SDIIMSDYLPRAPSPRLS 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published_Applications-AA:*
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10: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2318	100.0	451	10	US-09-860-797-2
2	2318	100.0	451	10	US-09-740-033-2
3	821.5	35.4	419	10	US-09-740-033-4
4	438.5	18.9	368	10	US-09-768-703-2
5	349	15.1	359	10	US-09-989-861-19
6	341.5	14.7	359	10	US-09-829-631A-13
7	340	14.7	359	10	US-09-951-622-13
8	329.5	14.2	437	10	US-09-829-631A-8
9	326.5	14.1	400	10	US-09-895-211-6
10	326.5	14.1	400	10	US-09-895-211-4
11	320	13.8	501	10	US-09-951-622-9
12	319.5	13.8	394	10	US-09-993-844-7
13	319.5	13.8	408	10	US-09-895-211-5
14	309.5	13.4	408	10	US-09-895-211-2
15	308	13.3	517	10	US-09-951-622-10
16	305	13.2	497	12	US-10-052-589-2
17	300	12.6	466	10	US-09-951-622-11
18	291.5	12.6	388	10	US-09-989-861-8
19	286.5	12.4	529	10	US-09-951-622-2

20	286	12.3	259	10	US-09-796-338A-23	Sequence 23, Appl
21	279.5	12.1	451	10	US-09-993-844-6	Sequence 6, Appl
22	271.5	11.7	291	10	US-09-829-631A-10	Sequence 10, Appl
23	270	11.6	445	10	US-09-989-861-16	Sequence 16, Appl
24	267.5	11.5	382	10	US-09-993-844-5	Sequence 5, Appl
25	264.5	11.4	222	10	US-09-911-005-4	Sequence 4, Appl
26	263	11.3	387	10	US-09-989-861-2	Sequence 2, Appl
27	263	11.3	406	10	US-09-989-861-4	Sequence 4, Appl
28	259	11.2	460	10	US-09-989-861-18	Sequence 18, Appl
29	250.5	10.8	390	10	US-09-160-116-19	Sequence 19, Appl
30	250	10.8	431	10	US-09-826-508-22	Sequence 22, Appl
31	250	10.8	431	10	US-09-899-532-2	Sequence 2, Appl
32	247	10.7	601	10	US-09-782-980-84	Sequence 84, Appl
33	247	10.7	601	10	US-09-884-430-8	Sequence 8, Appl
34	243	10.5	505	9	US-10-029-009-21	Sequence 21, Appl
35	241.5	10.4	428	10	US-09-292-973-4	Sequence 4, Appl
36	241	10.4	488	9	US-10-029-009-9	Sequence 9, Appl
37	239	10.3	518	10	US-09-804-551B-8	Sequence 8, Appl
38	238.5	10.3	481	8	US-08-681-219-31	Sequence 31, Appl
39	238.5	10.3	481	10	US-09-919-497-72	Sequence 72, Appl
40	236	10.2	398	10	US-09-796-338A-17	Sequence 17, Appl
41	236	10.2	398	10	US-09-897-201-2	Sequence 2, Appl
42	234	10.1	402	12	US-10-077-874-2	Sequence 2, Appl
43	234	10.1	425	10	US-09-961-848-2	Sequence 2, Appl
44	233.5	10.1	427	10	US-09-730-931-2	Sequence 2, Appl
45	233	10.1	370	12	US-10-044-592-12	Sequence 12, Appl

ALIGNMENTS

```
RESULT 1
US-09-860-797-2
: Sequence 2, Application US/09860797
: Patent No. US20020064825A1
: GENERAL INFORMATION:
: APPLICANT: Marillyn Evelyn Lewis
: APPLICANT: Nicola Melande Robas
: TITLE OF INVENTION: NO. US20020064825A1el Polypeptide
: FILE REFERENCE: PCS10924APME
: CURRENT APPLICATION NUMBER: US/09/860,797
: PRIOR FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: GB 0012248.1
: PRIOR FILING DATE: 2000-05-19
: PRIOR APPLICATION NUMBER: GB 0107394.9
: PRIOR FILING DATE: 2001-03-23
: PRIOR APPLICATION NUMBER: US 60/211,421
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/283,441
: PRIOR FILING DATE: 2001-04-12
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 451
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-860-797-2
Query Match      100.0%   Score 2318:   DB 10:   Length 451:
Best Local Similarity 100.0%:   Pred. No. 3.6e-189:
Matches 451:   Conservative 0:   Mismatches 0:   Indels 0:   Gaps 0:
OY 1 MESSPPIQSSGNSSTLGRVPQPGSTAGVPEGLRVDVASESYALFFMLLDITAVAGN 60
Db 1 MESSPPIQSSGNSSTLGRVPPGPGSTAGVPEGLRVDVASESYALFFMLLDITAVAGN 60
OY 61 AAVAAVIAKTPALKKFFVFLCLVDLLAALTLPPLAMISSALFDHALFEVACRYLTF 120
Db 61 AAVAAVIAKTPALKKFFVFLCLVDLLAALTLPPLAMISSALFDHALFEVACRYLTF 120
OY 121 LSVCFSLATISVSAINVERYYVHPKRYEVRRTGLGVASVLGVWVKALAMASVPLTG 180
Db 121 LSVCFSLATISVSAINVERYYVHPKRYEVRRTGLGVASVLGVWVKALAMASVPLTG 180
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Db 121 LSVCFVSLAIISSVAINVERYYYVHPRMYEVRMTLGLVASVLGVWVKALAMASVPLG 180
QY 181 RVSMEEGAPSVPPGCSIQMWSHSAVCOLFVYVFAVLFLPLLILLVYCSMFRRARVAA 240
Db 181 RVSMEEGAPSVPPGCSIQMWSHSAVCOLFVYVFAVLFLPLLILLVYCSMFRRARVAA 240
QY 241 QHGPPLPTWMTPTPORSSELSRSSTMTWSSGAPOTTPHRTFGGKAAVLLAVGGQFLLCW 300
Db 241 QHGPPLPTWMTPTPORSSELSRSSTMTWSSGAPOTTPHRTFGGKAAVLLAVGGQFLLCW 300
QY 301 LPYFSFLHYVALSAQPISTQGVESVYTWIGYFCFTSNPFYGCINROIIRGELSKQFVCF 360
Db 301 LPYFSFLHYVALSAQPISTQGVESVYTWIGYFCFTSNPFYGCINROIIRGELSKQFVCF 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSSESWSRPLSPKQEPVAVDFRIPGOIAE 420
Db 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSSESWSRPLSPKQEPVAVDFRIPGOIAE 420
QY 421 ETSEFLEQULTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLEQULTSDIIMSDSYLRPAASPRLES 451

RESULT 2

US-09-740-033-2
; Sequence 2, Application US/09740033
; Patent No. US20020100067A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1001056
; CURRENT APPLICATION NUMBER: US/09/740,033
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Human
US-09-740-033-2

Query Match 100.0%; Score 2318; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 3.6e-189;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTIGRVOTPEPSTASGVPEYGLDVASESYALFFMILLDLITAVAGN 60
Db 1 MESSPIPOSSGNSSTIGRVOTPEPSTASGVPEYGLDVASESYALFFMILLDLITAVAGN 60
QY 61 AAMVAVIAKTPALRKRFVFEVHCLVDLAALTLPMLAMLSLSDHDLGEGVACRYLYLF 120
Db 61 AAMVAVIAKTPALRKRFVFEVHCLVDLAALTLPMLAMLSLSDHDLGEGVACRYLYLF 120
QY 121 LSVCFVSLAIISSVAINVERYYYVHPRMYEVRMTLGLVASVLGVWVKALAMASVPLG 180
Db 121 LSVCFVSLAIISSVAINVERYYYVHPRMYEVRMTLGLVASVLGVWVKALAMASVPLG 180
QY 181 RVSMEEGAPSVPPGCSIQMWSHSAVCOLFVYVFAVLFLPLLILLVYCSMFRRARVAA 240
Db 181 RVSMEEGAPSVPPGCSIQMWSHSAVCOLFVYVFAVLFLPLLILLVYCSMFRRARVAA 240
QY 241 QHGPPLPTWMTPTPORSSELSRSSTMTWSSGAPOTTPHRTFGGKAAVLLAVGGQFLLCW 300
Db 241 QHGPPLPTWMTPTPORSSELSRSSTMTWSSGAPOTTPHRTFGGKAAVLLAVGGQFLLCW 300
QY 301 LPYFSFLHYVALSAQPISTQGVESVYTWIGYFCFTSNPFYGCINROIIRGELSKQFVCF 360
Db 301 LPYFSFLHYVALSAQPISTQGVESVYTWIGYFCFTSNPFYGCINROIIRGELSKQFVCF 360
QY 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSSESWSRPLSPKQEPVAVDFRIPGOIAE 420
Db 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSSESWSRPLSPKQEPVAVDFRIPGOIAE 420

Db 361 KPAPEEELRLPSREGSIEENFLQFLOGTGCPSSESWSRPLSPKQEPVAVDFRIPGOIAE 420
QY 421 ETSEFLEQULTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLEQULTSDIIMSDSYLRPAASPRLES 451

RESULT 3

US-09-740-033-4
; Sequence 4, Application US/09740033
; Patent No. US20020100067A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1001056
; CURRENT APPLICATION NUMBER: US/09/740,033
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Oryzias latipes
US-09-740-033-4

Query Match 35.4%; Score 821.5; DB 10; Length 419;
Best Local Similarity 42.8%; Pred. No. 3e-62;

Matches 182; Conservative 78; Mismatches 140; Indels 25; Gaps 10;

QY 9 SSGNSST--LGRVQPTPEPSTASGVPEVGL----RDVASESYALFFMILLDLITAVAGNAA 62
Db 8 SISNFTSGLEGPHTVPE-----PDVGVVTSQSQGMKDLFGLFQCVITLNTLALTANTG 59
QY 63 VMVAVIAKTPALRKRFVFEVHCLVDLAALTLPMLAMLSLSDHDLGEGVACRYLYLF 122
Db 60 VMVAVIAKTPALRKRFVFEVHCLVDLAALTLPMLAMLSLSDHDLGEGVACRYLYLF 119
QY 123 VCFVSLAIISSVAINVERYYYVHPRMYEVRMTLGLVASVLGVWVKALAMASVPLG 182
Db 120 VFLIWLSTLITTAISVERYYYVHPRMYEVRMTLGLVASVLGVWVKALAMASVPLG 179
QY 183 SWEAGAPSVPPGCSIQMWSHSAVCOLFVYVFAVLFLPLLILLVYCSMFRRARVAA 242
Db 180 PYGHOSSIAASHCSLHSHSLRGVFAVLEFCVIFLAPVVIISVYSAVVKVARSALQ 239
QY 243 GP-LPTWMT--PRQSESLSSNSTMTWSSGAPOTTPHRTFGGKAAVLLAVGGQFL 298
Db 240 VPAPVPTWADASPDKRDSINSQTTITITRTLPQRLSPERAFSGKAAVLLAVGGQFL 299
QY 299 CMLPYFSFLHYVALSAQPISTQGVESVYTWIGYFCFTSNPFYGCINROIIRGELSK-QFV 357
Db 300 CMLPYFSFLHYVALSAQPISTQGVESVYTWIGYFCFTSNPFYGCINROIIRGELSK-QFV 359
QY 358 CFPKPAPEEELRLPSREGSIEENFLQFLOGTGCPSSESWSRPLSPK-QEPVAVDFRIP 416
Db 360 CVYQGPV---ELGPSLSLEGQOENFLQFLOGTGCPSSESWSRPLSPK-QEPVAVDFRIP 414
QY 417 QIAEE 421
Db 415 QIRPEE 419

RESULT 4

US-09-768-703-2
; Sequence 2, Application US/09768703
; Patent No. US20020098538A1
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: MICHALOVICH, DAVID
; TITLE OF INVENTION: 7TM RECEPTOR (AXOR23)

QY 191 VPGCSLOWSHSAYCOLFVVVFAVLYFLBLLLLVYVCSMFVARYAAMQHGLPTWME 250
175 VPGCRILASLP-----FVLVASGLFELPSGALICFTYCHLLAARQAQVVASLTGMA 229
QY 251 TPNORSESLS---SRSTWMTSSGAPOTTPHRTGGKAAVYLLAVGOFLLCWLPTFSFH 307
230 S--QASSETLOVPRSPAGVGSADSRRLATKSSRGLKASMTGLILLGMFEVTLPEFVAN 287
QY 308 LVAVALSAQPISTGOVESVMTWIGVFCFTSNPFYGCUNRQIRGELSQQVCFKRP----- 362
288 IVQAV-CDCTISPLFD-VLTMWLGICNSTMNPITYPLFMDLFRALGRFLPCPRCPREP 345
QY 363 -----APEEL-----RLPSREGSIEENFLOFLQGTGC---PSESWSRPL 401
346 AMRHHHCAPLTAAPGALAVSRCCRCRRTQIRTOQAQAAPRACGSRSCFLANPR 405
QY 402 SPKQEP 407
406 TPRCP 411

RESULT 7

US-09-951-622-13
Sequence 13, Application US/09951622
Patent No. US20020106734A1
GENERAL INFORMATION:
APPLICANT: Daniel R. Soppet et al.
TITLE OF INVENTION: ADRENERGIC RECEPTOR
FILE REFERENCE: PFI28D2C1
CURRENT APPLICATION NUMBER: US/09/951,622
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/339,244
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 09/030,582
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 08/467,568
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/US94/09051
PRIOR FILING DATE: 1994-08-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 359
TYPE: PRT
ORGANISM: human
US-09-951-622-13

Query Match 14.7%; Score 340; DB 10; Length 359;
Best Local Similarity 28.0%; Pred. No. 1.7e-21;

Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

QY 49 MLLDLTAVGNAVAVIKTRPALRKEV--FVHCLVDVLLAALTLPLAMSSSLFD 106
25 LAVLILITVAGNVAVCLAVGLNRLNLTNCFTVSLAITDGLGLVLP-----SAIYQ 79
QY 107 HAL---EGEVACRLYLELSCFVSLATLSAIVNERYVYVHPMRREVMTGLVAVSL 163
80 LSGKNSEFGKFCNITSLDWMCTASTILNLFMTSLDRYCAVMDPKRPVLTVEYRAVSL 139
QY 164 VGWVAKALMASVVP-LGRVSWEGAPS--VPGCSLOWSHSAYCOLFVVVFAVLYFLP 220
140 VLIWVISTLSPFSLIHGWNRSNRTSKGNTJTSKCVQVN-----EYGLVDGLVTFYLP 194
QY 221 LLLILVYVCSMFVARYAAMQHGLPTWMTTPRORSESLSRSTWMTSSGAPOTTPHRTF 280
195 LLMCTTYRIFVAVDAQARINHISWKA-----TI 227
QY 281 GCGKAHVLLAVGOFLLCWLPEFSEFLVYALSAQPISTGOVESVMTWIGVFCFTSNPFF 340
228 REKRAVTLAAVNGAFLLICFPYFAVYRGLGDDAINEVLEAVLWGLVANSALNPIL 287
QY 341 YGCLNRINGELSKQFVCFKPAPEELRLPSREG---SIEENFLO 383

Db 288 YALNRDFRTGYOQLFCC-----RLANRSHKTSLSRNASQ 323

US-09-829-631A-8
Sequence 8, Application US/09829631A
Patent No. US20020091235A1
GENERAL INFORMATION:
APPLICANT: Sibley, David R.
APPLICANT: Monsma, Frederick J.
APPLICANT: Hamblin, Mark
TITLE OF INVENTION: The 5T-B17 Serotonin Receptor
FILE REFERENCE: NIH047.1CPI1
CURRENT APPLICATION NUMBER: US/09/829,631A
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 08/428,242
PRIOR FILING DATE: 1995-09-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 437
TYPE: PRT
ORGANISM: Rat
US-09-829-631A-8

Query Match 14.2%; Score 329.5; DB 10; Length 437;
Best Local Similarity 27.3%; Pred. No. 1.7e-20;

Matches 128; Conservative 65; Mismatches 181; Indels 95; Gaps 19;

QY 2 ESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASESYALFEMLLDITAVAGNA 61
4 EPGV-----NSSR---PAMGPBPAPG-----GSGWMAALCVIYVTLA-AANS 45
QY 62 AVAAVIAKTPLARKE--VEVHCLVDVLLAALTLPLAMSSSLFDHALFGEVACRLYL 119
46 LLIIVICTOPAVRNTSNFELVSLFTSDLMVGLVYMPAML--NALYGRVLAGRLCULMT 103
QY 120 FLSCVPSLALISVSAIVNERYVYVHPMRREVMTGLVAVYGVWAKALMASVPL 179
104 AFDVCCSASILNLCISLDRYLLILSLPKLMTAPRALALILGWSLAALASPLPL 163
QY 180 GRVSWEE-GAPVVP-PGCSLOWSHSAYCOLFVVVFAVLYFLBLLLLVYVCSMF 232
164 --LGMHELKKAFTAPAG-----QCRILASLPFLVASGVTFPLPSGALICFTYCRIL 212
QY 233 RVARVAAAMQHGLPTW-----ETPRORSESLSRSTWMTSSGAPOTTPHRTFG 281
213 LAARKQAVVAVASLTGTAGALETLOVPRTPRGMESADSRRLATKHSKAL----- 264
QY 282 GGRAAVVLLAVGOFLLCWLPEFSEFLVYALSAQPISTGOVESVMTWIGVFCFTSNPFF 341
265 --KASLTGLILGMFEVYTWLPFFVANIQAQV-CDCTISPLFD-VLTMWLGICNSTMNPITY 320
QY 342 GCUNRQIRGELSQQV-----CFKPAPEELRLP-----S 372
321 PLMRDPRKALGR-FLHASTVPRSTGQCLPLHYVDSLQROGTRPQQLVALLPLPNSDS 379
QY 373 REGSIEENFLOFLQGTGCPESEWSRPLSPKQEPVAVDRIRIQALAE 421
380 DSASGTSGLQTLTAOLLLPGEA--TRDPPPTTRATVNVNFVDSVEPE 426
RESULT 9
US-09-895-211-4
Sequence 4, Application US/09895211
Patent No. US20020127639A1
GENERAL INFORMATION:
APPLICANT: Hutton and Williams
APPLICANT: Emoline, Laurent
TITLE OF INVENTION: INTRON/EXON STRUCTURE OF THE HUMAN AND MOUSE BETA3 ADRENERGIC
FILE REFERENCE: 58769.000011

Query Match 13.4%: Score 309.5; DB 10; Length 408;
Best Local Similarity 29.4%: Pred. No. 8e-19;
Matches 112; Conservative 60; Mismatches 162; Indels 47; Gaps 17;

QY 4 SPIPOSSGNSSTLGRVPPQ--GPSTA--SGVEVGLRDVASESVALFEMLLDLTAAG 59
DB 2 APMPH--ENSLAMPDPTLAPNTANTSGLP--GVPMAALAGALLAVLATIGV-- 54
QY 60 NAAVAVIAKTPALRKF--VFVFLCLVDLLAALTMLPLAMSSSALFDHALGEVACRL 117
DB 55 NLVIAIATMTPLQMTNTEFVSLAAADLVAGLLVPPA--ATLALTGHMPGAGCCEL 112
QY 118 YLEFLSCFVSALTSYSAINVERYYVHBMREVRMTGLVASVGVVWVKAAMASVP 177
DB 113 WTSVDVLCYASLETICALAVDRILAVTNPLRIGALVTKCAATVAVLVWVSAASFPAP 172
QY 178 VLGRVSWEGAPSVP-----PGCSLWMSHSAVCQLFVVFAVLFLPLLLVYCS 230
DB 173 IMSQ--WMRGVADAEARQCHSNPRCCAFASQMPY----VLLSSVSPLYPLVLMLEFYAR 226
QY 231 MRVA----RYAAMQHPLEPTMETPRQSESSR--STWNTSSGAP-----QTPH 277
DB 227 VFVVAATROLRLRGELGRPPP--EESPPASRSLAPAPVGTCAPEGVPAQGRPARLLPL 285
QY 278 RFRGGKAAVVLLAVGGPFLCWLPEFSPHLYALSAQPISTGQVESVYTWIGFCTSN 337
DB 286 REH--RALCTGLGTMGTFLCWLPEFLANVLALGPPSLVPGAPLALMWLGYANSAPN 342
QY 338 PEFYGCILNRQINGELSKQFVC 358
DB 343 PLTY-CRSPDFRSAPF-RRLIC 361

RESULT 15
US-09-951-622-10
; Sequence 10, Application US/09951622
; Patent No. US20020106734A1
; GENERAL INFORMATION:
; APPLICANT: Daniel R. Soppet et al.
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; FILE REFERENCE: PF128D2C1
; CURRENT APPLICATION NUMBER: US/09/951,622
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/339,244
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 09/030,582
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 08/467,568
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US94/09051
; PRIOR FILING DATE: 1994-08-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 517
; TYPE: prt
; ORGANISM: human
US-09-951-622-10

Query Match 13.3%: Score 308; DB 10; Length 517;
Best Local Similarity 25.9%: Pred. No. 1.5e-18;
Matches 117; Conservative 84; Mismatches 167; Indels 84; Gaps 21;

QY 24 GP---STAGGVPEVGLRDVASESVALFEMLLDLTAAGNAAMAVIAKTPALR--KFPV 78
DB 27 GPMQTSNSTLPLQDLITRAISVGLVGAFLP--AIVGNILVILSVACNRHLRTPTNYF 83
QY 79 VFHLCVLDLALTLMPPLAMSSSALFDHALPEVACRLYFLSVCFVSLAITSVAINV 138
DB 84 IYNLAADLFLSTVLPFS--AALEVAGVWVIGRICDIAAADVLCCTPASTILCAISI 141
QY 139 ERYYYVHMRVEVRTLGLVASVLVGVWVKALAMASVPVLGRVSWEGAPSVPGCSLQ 198

DB 142 DRYIGVRSIQYFTVTRRAAILALLSVWLSVVISIGPLG---WKEPAPNDKEGVT 198
QY 199 WSHSAYCQLEFVVFAVL-YFLPLLLLVVYCSMFVYAR--VAAMQHPLEPTMETPRQ- 254
DB 199 E-----EPYALFSSISGSFYIPLAVILVYCHVYIAKRTKRLNLEAGVKE-MSNSKEL 251
QY 255 --RSESSSRSTWVTSSGAPQTPPHRTFG-----GCKAAVLLAVGGPFLCWLPPF 304
DB 252 TLRIHSKNFHEDTLSTKAKGHNPRSSIAVKLFESREKKAATLGLVGMFTLCWLPPF 311
QY 305 SFHLYALSAQPIST-----GOVESVYTWIGFCEFTSNPEFYGCILNRQINGELSKOF 356
DB 312 -----IAL--PLGSLESTLKPPDAVFKYVFWLGTNNSCLNPLIYCCSSK----EKKRAF 359
QY 357 V-----CFKPPAPEEBRLP-----SREGSIE--ENLQPLQGTG-CPSSEWVS 398
DB 360 VRIIGCCRCGRRRRRRRRLGCGCAYYRPWTRGCSLSERSQSRKDSLDDSGSLSGQRTL 419
QY 399 PLRSP-----KQPPAV-----DFRIPOQI 418
DB 420 PSASPSBGYIGRGAAPPVELCAPPEWKAAPGAL 451

Search completed: December 10, 2002, 09:59:34
Job time : 13 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

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Run on:      December 10, 2002, 09:53:05 ; Search time 40 Seconds
              (without alignments)
              1502.401 Million cell updates/sec
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Title: US-09-838-028-2
Perfect score: 2318
Sequence: 1 MESSDIPQSSGNSSTLGRVP.....SDIIMSDYLRLPASPRLLES 451
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2318	100.0	451	22	AAE12024	Human G-protein cc
2	2318	100.0	451	22	AAU07900	Human serotonic-11
3	2318	100.0	451	22	AAU08410	Human histamine H2
4	2318	100.0	451	22	AAU08367	Human G-protein cc
5	2318	100.0	451	22	AAU684123	Human G-protein cc
6	2318	100.0	451	23	ABR841539	Human G-protein cc
7	2318	100.0	451	23	AAU787332	Novel human GPCR,
8	2318	100.0	451	23	AAAM50637	Human G protein cc
9	2318	100.0	451	23	AAO14014	Human G-protein cc
10	2318	100.0	451	23	AAU74909	Human acid sequen

1.1	2318	100.0	451.23	AAU11895
1.2	2318	100.0	451.23	AAE17073
1.3	2318	100.0	451.23	ABR05445
1.4	2318	100.0	869.22	AAU04386
1.5	2317	100.0	451.23	AAU11896
1.6	2313	99.81	451.22	AAU04382
1.7	2204	95.1	449.23	AAU14015
1.8	2185	94.3	449.23	AAAS0638
1.9	1472	63.5	279.22	AAAG6645
2.0	1276	55.0	252.17	AAAP0695
2.1	1276	55.0	252.17	AAAR1232
2.2	821.5	35.4	419.23	ABBR1540
2.3	692	29.9	368.22	AAOC0587
2.4	438.5	18.9	368.22	AAAB19523
2.5	438.5	18.9	368.21	AAAT1293
2.6	438.5	18.9	368.21	AAAB02827
2.7	438.5	18.9	368.22	AAU04288
2.8	438.5	18.9	368.22	AAAG64303
2.9	438.5	18.9	368.22	AAAT70142
3.0	438.5	18.9	368.23	AAE19359
3.1	438.5	18.9	368.23	AAU15903
3.2	343.5	15.1	440.22	ABBS06532
3.3	347	15.0	348.18	AAAB0551
3.4	347	15.0	348.18	AAAT1712
3.5	346	14.9	359.20	AAAO0080
3.6	341	14.7	359.20	AAU10902
3.7	340	14.7	359.20	AAAY00889
3.8	340	14.7	359.21	AAAT57172
3.9	340	14.7	359.23	AAU10901
4.0	340	14.7	400.14	AAAR12501
4.1	335.5	14.5	405.15	AAAR05215
4.2	333	14.4	565.22	AAU05409
4.3	332.5	14.3	572.15	AAAR3071
4.4	332.5	14.3	572.15	AAAR8681
4.5	332.5	14.3	572.16	AAAR90039

ALIGNMENTS

RESULT 1	
AAE12024	
ID	AAE12024 standard; Protein; 451 AA

AC...AAE12024;
XX
DT 18-DEC-2001 (first entry)

Human G-protein coupled receptor, GCRC-3

KW Human; G-protein coupled receptor; GCRC; gene therapy;
KW proteasome analysis; cell proliferative disorder; arteriosclerosis;
KW cancer; neurological disorder; Huntington's disease; Parkinson's disease;
KW cardiovascular disorder; atherosclerosis; congestive heart failure;
KW gastrointestinal disorder; gastritis; nausea; autoimmune; anaemia;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW metabolic disorder; diabetes; obesity; viral infection; drug screening;
KW chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
KW vincristine.

Homo sapiens

FH	Key	Location/Qualifiers
17		17

FT	/label= Transmembrane_domain
EM	306-339
Domain	

FT	Domain	/label= Transmembrane_domain
FT	398	306

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XX      /label= Transmembrane_domain
XX

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PN WO2001/2836-A2
XX

FD 04-001-2001

XX 29-MAR-2001: 2001MO-US10436.
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 XX 29-MAR-2000: 2000US-193051P.
 PR 06-APR-2000: 2000US-195155P.
 PR 20-APR-2000: 2000US-199084P.
 PR 28-APR-2000: 2000US-200551P.
 PR 05-MAY-2000: 2000US-202278P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Policky JL, Tribouley CM, Tang YT, Baughn MR, Graul R, Khan FA;
 PI Nguyen DB, Patterson C, Lai P, Au-Young J, Yang J, Hatalla A;
 PI Walla NK, Das D;
 XX
 DR WPI: 2001-616472/71.
 DR N-PSDB: AAD19579.
 XX
 PT New human G-protein coupled receptors, useful for treatment and
 PT diagnosis of e.g. cell proliferation, also screening for specific
 PT modulators, and related nucleic acid
 XX
 PS Claim 1: Page 104-105; 11pp: English.
 XX
 CC The present sequence is a human G-protein coupled receptor, GCRC-3
 CC protein. The GCRCs are used for treating or preventing disorders
 CC associated with decreased expression of functional GCRC, and for
 CC identifying specific agonists and antagonists, also binding agents
 CC and modulators. They can also be used for generating specific antibodies
 CC and for proteosome analysis. Disorders that can be treated include
 CC cell proliferative disorders, e.g., arteriosclerosis and cancer,
 CC neurological disorders, e.g., Huntington's disease and Parkinson's
 CC disease, cardiovascular disorders, e.g., atherosclerosis and congestive
 CC heart failure, gastrointestinal disorders, e.g., gastritis and nausea,
 CC autoimmune/inflammatory disorders, e.g., acquired immunodeficiency
 CC syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and
 CC obesity and viral infections. Nucleic acids that encode GCRC are
 CC used for identifying agents that alter its expression, for assessing
 CC toxicity of test compounds, and as sources of primers and probes for
 CC diagnostic detection of GCRC DNA and of therapeutic antisense and
 CC ribozyme sequences. They can also be used in gene therapy, for
 CC chromosomal mapping, and for recombinant production of GCRC. The
 CC antibodies are useful for diagnosis and monitoring of diseases
 CC associated with GCRC expression, for detecting and purifying GCRC,
 CC and as therapeutic agents and for drug screening.
 CC
 SO Sequence 451 AA:
 Query Match 100.0%; Score 2318; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEGLRDVASESALFPMLLDTANAAGN 60
 DB 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEGLRDVASESALFPMLLDTANAAGN 60
 QY 61 AAVAVIAKPKALRKFFVFNHLCVLDLALTLMLPLAMLSAFLDHALGEGVACRLYLF 120
 DB 61 AAVAVIAKPKALRKFFVFNHLCVLDLALTLMLPLAMLSAFLDHALGEGVACRLYLF 120
 QY 121 LSVCFVSLATLSVAINVERYYVHPMRK EVMRTGLVASVILGVWVKALAMASVPLG 180
 DB 121 LSVCFVSLATLSVAINVERYYVHPMRK EVMRTGLVASVILGVWVKALAMASVPLG 180
 QY 181 RVMEBEGAPVPKGCSTQWHSATCOLFVYVFNFLPLLLLVYVCSFRARARAAAM 240
 DB 181 RVMEBEGAPVPKGCSTQWHSATCOLFVYVFNFLPLLLLVYVCSFRARARAAAM 240
 QY 241 QHGPLPTMWTPTKORSSLSRSTMTWSSGAPOTTPHRTFGGKAAAVLLAVGGQFLCW 300
 DB 241 QHGPLPTMWTPTKORSSLSRSTMTWSSGAPOTTPHRTFGGKAAAVLLAVGGQFLCW 300
 QY 301 LPYFSFLVVALSAQPISTGOVESVWTWIGYFCTSNPFYGCILNROI RGLSKQFVCF 360

DB 301 LPYFSFLVVALSAQPISTGOVESVWTWIGYFCTSNPFYGCILNROI RGLSKQFVCF 360
 QY 361 KPAPEEELRLPBRGCSIEENFLQLOGTGCPSESWRPLPSPKQEPNPAVDFRPGQIAE 420
 DB 361 KPAPEEELRLPBRGCSIEENFLQLOGTGCPSESWRPLPSPKQEPNPAVDFRPGQIAE 420
 QY 421 ETSEFLQOLTSIDTMSDYLRPAASPRLES 451
 DB 421 ETSEFLQOLTSIDTMSDYLRPAASPRLES 451
 RESULT 2
 ID AAU07900 standard; Protein: 451 AA.
 AC AAU07900;
 DT 18-DEC-2001 (first entry)
 DE Human serotonin-like G protein-coupled receptor (5-HT-GPCR).
 KW Human: serotonin-like G protein-coupled receptor; 5-HT-GPCR;
 KW peripheral nervous system; central nervous system; PNS; CNS;
 KW brain injury; mood disorder; anxiety disorder; sleep disorder;
 KW neurogenic; myopathic disorder; neurodegenerative disorder;
 KW tranquilizer; nootropic; neuroprotective; antiparkinsonian;
 KW analgesic; cerebroprotective.
 OS Homo sapiens.
 PN WO200170967-A2.
 PD 27-SEP-2001.
 PX 19-MAR-2001: 2001MO-EP03117.
 PX 20-MAR-2000: 2000US-190104P.
 PX 12-JUN-2000: 2000US-210975P.
 PR 14-DEC-2000: 2000US-255110P.
 PA (FARB) BAYER AG.
 PI Ramakrishnan S;
 PT
 DR WPI: 2001-611498/70.
 DR N-PSDB: AAS12583.
 PT
 PT New polynucleotide encoding a polypeptide which regulates, prevents and
 PT treats diseases of the peripheral or central nervous system including
 PT Alzheimer's Disease, comprises the human serotonin-like G
 PT protein-coupled receptor polynucleotide -
 XX
 PS Claim 1: Fig 2; 88pp; English.
 XX
 CC The present invention relates to the isolation of a novel DNA sequence
 CC encoding a human serotonin-like G protein-coupled receptor (5-HT-GPCR)
 CC polypeptide. The sequences of the invention are useful for screening for
 CC agents which decrease the activity of 5-HT-GPCR or for identifying agents
 CC which regulate the activity of 5-HT-GPCR. A reagent that modulates the
 CC activity of 5-HT-GPCR is useful for detecting 5-HT-GPCR in a biological
 CC sample and for reducing the activity of 5-HT-GPCR in a cell. A
 CC pharmaceutical composition comprising such a reagent is useful for
 CC preventing or ameliorating disorders of the peripheral or central nervous
 CC system, preferably primary or secondary disorders after brain injury,
 CC mood disorders, anxiety disorders, disorders of thought and volition,
 CC sleep disorders, diseases of the motor unit such as neurogenic and
 CC myopathic disorders, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease) or disorders leading to peripheral and
 CC chronic pain. The coding sequence of 5-HT-GPCR polynucleotide is useful
 CC for generating antisense oligonucleotides or ribozymes which specifically
 CC bind to mRNA transcribed from the 5-HT-GPCR polynucleotide. These
 CC antisense oligonucleotides are useful for modulating 5-HT-GPCR gene

CC expression. Polynucleotide sequences encoding for 5-HT-GPCR may be used
 CC in gene therapy. The present sequence represents the novel human
 CC 5-HT-GPCR polypeptide of the invention.

XX Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEYGLRDVASSEVALFFMLLDTTAVAGN 60
 DB 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEYGLRDVASSEVALFFMLLDTTAVAGN 60
 QY 61 AAVMAVIAKTPALRKFEVFNHCLVDLAALTPLMLSSALFDHALGEGVACRLYL 120
 DB 61 AAVMAVIAKTPALRKFEVFNHCLVDLAALTPLMLSSALFDHALGEGVACRLYL 120
 QY 121 LSYCFVSLALISVSAINVERYYVHPMRKEVRMTGLVASVLYGVWVKALAMASVPLG 180
 DB 121 LSYCFVSLALISVSAINVERYYVHPMRKEVRMTGLVASVLYGVWVKALAMASVPLG 180
 QY 181 RVSMEGAPSVPPGCSLQWMSHAYCQLFVVFAVLYFLPLLLLVYCSMFVARVAAM 240
 DB 181 RVSMEGAPSVPPGCSLQWMSHAYCQLFVVFAVLYFLPLLLLVYCSMFVARVAAM 240
 QY 241 QHGPLPTWMTTPRORSLSLSRSTMTWSSGAPQTPHRTGGGKAANVLLAVGGQFLCW 300
 DB 241 QHGPLPTWMTTPRORSLSLSRSTMTWSSGAPQTPHRTGGGKAANVLLAVGGQFLCW 300
 QY 301 LPFSEFLIYALSAOPISTGOVESVWVWIGYFCFTSNPFYGCINROIRGELSKQFCFF 360
 DB 301 LPFSEFLIYALSAOPISTGOVESVWVWIGYFCFTSNPFYGCINROIRGELSKQFCFF 360
 QY 361 KPAPEELRLPSRGSIENEFLOFLOGTGCPSESWSRPLPSKQEPDAVDFRIPQIAE 420
 DB 361 KPAPEELRLPSRGSIENEFLOFLOGTGCPSESWSRPLPSKQEPDAVDFRIPQIAE 420
 QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
 DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 3

AAU08710 standard; Protein; 451 AA.

AC AAU08710;
 XX DT 18-DEC-2001 (first entry)

DE Human histamine H2-like G protein-coupled receptor polypeptide.

XX Histamine H2-like G protein-coupled receptor; histamine H2-like GPCR;
 KW digestive system; immune system; respiratory system; reproductive system;
 KW urinary system; peripheral nervous system; central nervous system; human;
 KW brain injury; mood disorder; anxiety; thought disorder; sleep disorder;
 KW motor unit disease; neurogenic disorder; myopathic disorder; neuroleptic;
 KW neurodegenerative disorder; psychotic disorder; cerebrovascular disorder;
 KW Alzheimer's disease; Parkinson's disease; muscle spasms; peripheral pain;
 KW chronic pain; tranquilliser; nootropic; neuroprotective; antiparkinsonian;
 KW analgesic; antidepressant; antiallergic; antiinflammatory; gene therapy;
 KW neuroprotective; vulnerrary.

OS Homo sapiens.

XX WO200170812-A2.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-EP03162.

XX 20-MAR-2000; 2000US-190554P.

PR 12-JUN-2000; 2000US-210734P.
 PR 14-DEC-2000; 2000US-255147P.

XX (FARB) BAYER AG.

XX Ramakrishnan S;

XX WPI: 2001-611486/70.

DR N-PSDB; AAS14725.

XX New human histamine H2-like G protein-coupled receptor polynucleotide
 PT and polypeptide which can be regulated for preventing, treating
 PT diseases of digestive, immune, respiratory, reproductive or central
 PT nervous system

PS Claim 1; Fig 2; 93pp; English.

CC The invention relates to a human histamine H2-like G protein-coupled
 CC receptor (GPCR) polypeptides and the nucleic acids encoding them. The
 CC sequences are useful for screening for agents which regulate the activity
 CC of histamine H2-like GPCR by contacting test compounds with the
 CC polypeptide and monitoring the activity. The polypeptides and their
 CC associated DNA sequences are useful for modulating the activity of a
 CC histamine H2-like GPCR in a disease of the digestive, immune,
 CC respiratory, reproductive, urinary, peripheral or central nervous system,
 CC especially a primary or secondary disorder after brain injury, disorder
 CC of mood, an anxiety disorder, a disorder of thought, a disorder of sleep,
 CC a disease of the motor unit, a neurogenic and myopathic disorder, a
 CC neurodegenerative disorder, a psychotic disorder, a cerebrovascular
 CC disorder, Alzheimer's disease, Parkinson's disease, muscle spasms or a
 CC disorder leading to peripheral and chronic pain. This sequence represents
 CC a human histamine H2-like GPCR polypeptide.

XX Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEYGLRDVASSEVALFFMLLDTTAVAGN 60
 DB 1 MESSPIPOSSGNSSTLGRVPOTPGPSTASGVPEYGLRDVASSEVALFFMLLDTTAVAGN 60
 QY 61 AAVMAVIAKTPALRKFEVFNHCLVDLAALTPLMLSSALFDHALGEGVACRLYL 120
 DB 61 AAVMAVIAKTPALRKFEVFNHCLVDLAALTPLMLSSALFDHALGEGVACRLYL 120
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 DB 121 LSYCFVSLALISVSAINVERYYVHPMRKEVRMTGLVASVLYGVWVKALAMASVPLG 180
 QY 181 RVSMEGAPSVPPGCSLQWMSHAYCQLFVVFAVLYFLPLLLLVYCSMFVARVAAM 240
 DB 181 RVSMEGAPSVPPGCSLQWMSHAYCQLFVVFAVLYFLPLLLLVYCSMFVARVAAM 240
 QY 241 QHGPLPTWMTTPRORSLSLSRSTMTWSSGAPQTPHRTGGGKAANVLLAVGGQFLCW 300
 DB 241 QHGPLPTWMTTPRORSLSLSRSTMTWSSGAPQTPHRTGGGKAANVLLAVGGQFLCW 300
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 DB 301 LPFSEFLIYALSAOPISTGOVESVWVWIGYFCFTSNPFYGCINROIRGELSKQFCFF 360
 QY 361 KPAPEELRLPSRGSIENEFLOFLOGTGCPSESWSRPLPSKQEPDAVDFRIPQIAE 420
 DB 361 KPAPEELRLPSRGSIENEFLOFLOGTGCPSESWSRPLPSKQEPDAVDFRIPQIAE 420
 QY 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451
 DB 421 ETSEFLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 4

ID	AAU04367	standard; Protein; 451 AA.
XX	AAU04367;	
AC	AAU04367;	
XX		
XX	23-OCT-2001	(first entry)
DT		
XX		
DE	Human G-protein coupled receptor, hrup13.	
XX		
KW	Human; G-protein coupled receptor; GPCR; hrup13; agonist;	
KW	inverse agonist; lung cancer.	
XX		
OS	Homo sapiens.	
XX		
XX	WO200136471-A2.	
PD	25-MAY-2001.	
XX		
PF	16-NOV-2000; 2000WO-US31509.	
XX		
PR	17-NOV-1999; 99US-0166088.	
PR	17-NOV-1999; 99US-0166099.	
PR	17-NOV-1999; 99US-0166369.	
PR	23-DEC-1999; 99US-0171900.	
PR	23-DEC-1999; 99US-0171901.	
PR	23-DEC-1999; 99US-0171902.	
PR	11-FEB-2000; 2000US-0181748.	
PR	14-MAR-2000; 2000US-0189258.	
PR	14-MAR-2000; 2000US-0189259.	
PR	10-APR-2000; 2000US-0195898.	
PR	10-APR-2000; 2000US-0195899.	
PR	10-APR-2000; 2000US-0196078.	
PR	28-APR-2000; 2000US-0200419.	
PR	12-MAY-2000; 2000US-0203630.	
PR	12-JUN-2000; 2000US-0210741.	
PR	12-JUN-2000; 2000US-0210982.	
PR	21-AUG-2000; 2000US-0226760.	
PR	26-SEP-2000; 2000US-0235418.	
PR	26-SEP-2000; 2000US-0235779.	
PR	20-OCT-2000; 2000US-0242332.	
PR	20-OCT-2000; 2000US-0242343.	
XX		
PA	(AREN-) ARENA PHARM INC.	
XX		
P1	Chen R, Dang HT, Lowitz KP;	
XX		
DR	WPI: 2001-355616/37.	
DR	N-PSDB; AAS07940.	
XX		
PT	Endogenous and non-endogenous versions of human G-protein coupled	
PT	receptors for direct identification of candidate compounds as agonists,	
PT	inverse agonists or partial agonists for use as therapeutic agents -	
XX		
PS	Claim 21; Page 98-100; 160pp; English.	
XX		
CC	The sequence represents a human G-protein coupled receptor (GPCR),	
CC	hrup13. The endogenous and non-endogenous, constitutively activated	
CC	versions of human G-protein coupled receptors (GPCR), are useful for	
CC	direct identification of candidate compounds as receptor agonists,	
CC	inverse agonists or partial agonists having applicability as therapeutic	
CC	agents for treating diseases related to GPCR, e.g. lung cancer.	
CC	Non-endogenous version of human GPCRs are also utilized in research	
CC	settings and in vitro and in vivo system, incorporating GPCRs can be	
CC	utilized to elucidate and understand the roles these receptors	
CC	play in the human condition, both normal and diseased.	
XX		
SO	Sequence 451 AA;	
XX		
Query Match	100.0%; Score 2318; DB 22; Length 451;	
Best Local Similarity	100.0%; Pred. No. 2,4e-228;	
Matches 451: Conservative	0; Mismatches 0; Indels 0; Gaps 0;	

Db	1	MESSSTIPSSSGNSSTLGVFPQTPEBSTASGVPEVGLNDVASEVALFPMLLDLTAVAGN	60
Qy	61	AAVMAVIAKTPALRRKFEVFHLCTVLDLAAITLPLAMLISSSALFDHALFGEVACRLYLE	120
Db	61	AAVMAVIAKTPALRRKFEVFHLCTVLDLAAITLPLAMLISSSALFDHALFGEVACRLYLE	120
Qy	121	LSVCVSLAIIISVSAINERYYYVHPRIKRYVRNTLGLVASYLVGVVWYKALMAASVPLG	180
Db	121	LSVCVSLAIIISVSAINERYYYVHPRIKRYVRNTLGLVASYLVGVVWYKALMAASVPLG	180
Qy	181	RYSMEGAPSVPPGCSLQMSHSAYCOLFVVVFAVLVFLPLLLTLVYVYCSMFYARVAAM	240
Db	181	RYSMEGAPSVPPGCSLQMSHSAYCOLFVVVFAVLVFLPLLLTLVYVYCSMFYARVAAM	240
Qy	241	QHGPLPTMETPPRORSESLSSRSTMTVTSAGAPQTTPHRTFGGKAAYVLAVAGQFLLCW	300
Db	241	QHGPLPTMETPPRORSESLSSRSTMTVTSAGAPQTTPHRTFGGKAAYVLAVAGQFLLCW	300
Qy	301	LPYFSEFHLVYALSAOPISTGQVESVYTWIGYFCTSNPFYGCINROIKGLSKQVYCF	360
Db	301	LPYFSEFHLVYALSAOPISTGQVESVYTWIGYFCTSNPFYGCINROIKGLSKQVYCF	360
Qy	361	KPAPEEELRLPSSREGSIENFLQFLOGTGCPSSESWSPRLPSPKOEPAPVDFRIPQIAE	420
Db	361	KPAPEEELRLPSSREGSIENFLQFLOGTGCPSSESWSPRLPSPKOEPAPVDFRIPQIAE	420
Qy	421	ETSEFLFEOQLTSDIIMSDSYLRPAASPRLES 451	
Db	421	ETSEFLFEOQLTSDIIMSDSYLRPAASPRLES 451	
RESULT 5			
AA64123	ID	AA64123 standard; Protein; 451 AA.	
XX	AC	AA64123;	
XX	DT	25-SEP-2001 (first entry)	
XX	DE	Human G protein-coupled receptor GPRV47.	
XX	XX		
KW	Human; guanosine triphosphate binding protein-coupled receptor;		
KW	G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;		
KW	GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;		
KW	Alzheimer's disease; cytosstatic; hepatotropic; nootropic;		
XX	neuroprotective; gene therapy; peptide therapy.		
OS	Homo sapiens.		
XX	XX		
PN	XX	WO200148188-A1.	
XX	PE	05-JUL-2001	
XX	PF	28-DEC-2000; 2000MO-JP09408.	
XX	PR	28-DEC-1999; 99JP-0375152.	
XX	PR	31-MAR-2000; 2000JP-0101339.	
XX	PA	(HELI-) HELIX RES INST.	
XX	PI	Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;	
XX	PI	Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;	
XX	DR	WPI; 2001-425662/45.	
XX	DR	N-PDSB; AAH73514.	
XX	XX		
PT	New DNA encoding guanosine triphosphate binding protein coupled		
PT	receptors and their expression products for screening potential		
PT	anticancer and nootropic drugs and in diagnosis of these diseases		
PS	Example 1; Page 126-129; 170pp; Japanese.		
XX	XX		

CC The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPR8, GPR12, GPR16
CC GPR21, GPR40, GPR47, GPR51, GPRV1 and GPRV2, and to the
CC genes encoding them. These genes and proteins and antibodies against
CC the protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease.
CC The present sequence is a G protein-coupled receptor of the invention.
CX

SQ Sequence 451 AA;

Query Match	100.0%	Score 2318;	DB 22;	Length 451;
Best Local Similarity	100.0%;	Pred. No. 2.4e-228;		
Matches 451; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MESSIPPOSSGSSSLTGVNPOTPGSRSTASGVPEVGLRBYASESVALFFMILLDLDTNAGN	60
Dp	1	MESSIPPOSSGSSSLTGVNPOTPGSRSTASGVPEVGLRBYASESVALFFMILLDLDTNAGN	60
Qy	61	AAYMAVIAKTPALRKFEVVFHCLCVDLLAALTLMPILAMLSSSALFDHALFGEVACRYLIF	120
Dp	61	AAYMAVIAKTPALRKFEVVFHCLCVDLLAALTLMPILAMLSSSALFDHALFGEVACRYLIF	120
Qy	121	LSVCFVSLAIIISVSAINVERYYYYVHPMRKEYERMTLGLVASVLYGVWVKALAMASVPLG	180
Dp	121	LSVCFVSLAIIISVSAINVERYYYYVHPMRKEYERMTLGLVASVLYGVWVKALAMASVPLG	180
Qy	181	RVSMEEGAPSVPPGCSLQMSHSAYCOLVVVFAVLYFLPLLLILLYVCSMEFRARVAAAM	240
Dp	181	RVSMEEGAPSVPPGCSLQMSHSAYCOLVVVFAVLYFLPLLLILLYVCSMEFRARVAAAM	240
Qy	241	QHGPPLTWMETPRRRESLSRSSTWVTSAGAPOTTPHRTFGGKAAYVLLAVGGOFLLCW	300
Dp	241	QHGPPLTWMETPRRRESLSRSSTWVTSAGAPOTTPHRTFGGKAAYVLLAVGGOFLLCW	300
Qy	301	LPYSEFHLVYALNSOPISITGOVESVYTWIIGFCFTSNFFFGCLNRQIRGLSLOQFCFF	360
Dp	301	LPYSEFHLVYALNSOPISITGOVESVYTWIIGFCFTSNFFFGCLNRQIRGLSLOQFCFF	360
Qy	361	KPAPEEELRLPSREGSIEENELQFLOGTGCPSESWSRPLSPKQPEAPVDFRILPGQIAE	420
Dp	361	KPAPEEELRLPSREGSIEENELQFLOGTGCPSESWSRPLSPKQPEAPVDFRILPGQIAE	420
Qy	421	ETSEFLBEOULTSDIIMSDSYLRPAASPLRES	451
Dp	421	ETSEFLBEOULTSDIIMSDSYLRPAASPLRES	451

RESULT 6
ARRR1539

ID ABB81539 standard; Protein; 451 AA.

AC ABB81539;

DT 03-SEP-2002 (first entry)

DE	Human G-protein coupled receptor protein SEQ ID NO:2
1	1
2	2
3	3
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6	6
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171	

KW Human; G-protein coupled receptor; GPCR; receptor; chromosome 1.

OS Homo sapiens.

PN WO200250272-A2

PD 27-JUN-2002.

PF 19-DEC-2001; 2001WO-US48547.

PR 20-DEC-2000; 2000US-0740033.

PA (PEKE) PE CORP NY.

PI Gan W, Di Francesco V, Beasley EM;

XX	
DR	WPI; 2002-500628/53.
DR	N-PSDB; ABN89471, ABN89472.

Novel isolated G-protein coupled receptor peptide useful for treating disorder characterized by absence of, inappropriate or unwanted expression of the receptor protein, and as immunogens to raise antibodies.

PS Claim 1; Fig 2A; 72pp; English

CC The present sequence represents a human G-protein coupled receptor (GPCR)
CC protein (1). (1) can be used in gene therapy. (1) can be used for
CC identifying a modulator of (1) by contacting (1) with an agent and
CC determining if the agent has modulated the function or activity of (1).
CC (1) is also useful for identifying an agent that binds to (1), by
CC contacting (1) with an agent and assaying the contacted mixture
CC to determine whether a complex is formed with the agent bound to (1).
CC (1) can be used in the treatment of a disorder characterised by the
CC absence of, inappropriate or unwanted expression of the receptor
CC protein. (1) is located to human chromosome 1.

50 Sequence 451 AA;

Query Match	100.0%	Score 2318;	DB 23;	Length 451;
Best Local Similarity	100.0%;	Pred. No. 2.4e-228;		
Matches 451; Conservative	0;	Mismatches	0;	Gaps 0;

Oy	1	MESSIPPOSSNSSNLTGIVPOTTPGPSTASGVPEVGLDVA	SESALEFMMLLDLDTAVAGN	60
Dd	1	MESSIPPOSSNSSNLTGIVPOTTPGPSTASGVPEVGLDVA	SESALEFMMLLDLDTAVAGN	60
Oy	61	AAVMAVIKTALEARKFEVFFHLCLVDLLAALTMLPLAM	SSSALFDHALFEVACRYLTF	120
Dd	61	AAVMAVIKTALEARKFEVFFHLCLVDLLAALTMLPLAM	SSSALFDHALFEVACRYLTF	120
Oy	121	LSVCVSTALITSVAINERYYYYVHHMRREVRTLCLVAS	YLVGVWVKALMAASPVLC	180
Dd	121	LSVCVSTALITSVAINERYYYYVHHMRREVRTLCLVAS	YLVGVWVKALMAASPVLC	180
Oy	181	RVSMEGASVPVPCGSLQWMSHSAQCOLFVVVFAVLYE	FLPLLTLVLYCGSMFRVARVAA	240
Dd	181	RVSMEGASVPVPCGSLQWMSHSAQCOLFVVVFAVLYE	FLPLLTLVLYCGSMFRVARVAA	240
Oy	241	OHGPLEPTMETPRORSBSLSRSTWMTSSGAPOTT	PHRTTGGGKAAYVLLAVGOFLLCW	300
Dd	241	OHGPLEPTMETPRORSBSLSRSTWMTSSGAPOTT	PHRTTGGGKAAYVLLAVGOFLLCW	300
Oy	301	LPYSEFHLIYVALSNOPISTGQVESVWMIWIGFCTT	SNPFYGCINROIKELSKOFVCF	360
Dd	301	LPYSEFHLIYVALSNOPISTGQVESVWMIWIGFCTT	SNPFYGCINROIKELSKOFVCF	360
Oy	361	KPAPEEELRLPSRSGSIEENFLQFLOGTGCPSESWS	RPLSPKQBPADVDFRIPQIAE	420
Dd	361	KPAPEEELRLPSRSGSIEENFLQFLOGTGCPSESWS	RPLSPKQBPADVDFRIPQIAE	420
Oy	421	ETSEFLQOULTSDIMSDSYLRPAASRLES	451	
Dd	421	ETSEFLQOULTSDIMSDSYLRPAASRLES	451	

RESULT 7
AAU79732

ID AAU79732 standard; Protein; 451 AA

AC AAU79732;

DT 15-JUL-2002 (first entry)

DE Novel human GPCR, PFI-018.

KW Human; G-protein coupled receptor; GPCR; obesity; diabetes; inflammation;
metabolic disease; neurological disease; psychotherapeutic; cancer;

KW urogenital disease; reproductive and sexual disease; tissue repair;
 KW dermatology; skin pigmentation; photosaging; frailty; osteoporosis;
 KW cardiovascular disease; gastrointestinal disease; infection; allergy;
 KW respiratory disease; sensory organ disorder; sleep disorder; hair loss;
 KW PFI-018; receptor.

OS Homo sapiens.
 PN EPI158002-A1.
 XX
 XX 28-NOV-2001.
 PD
 XX 16-MAY-2001; 2001EP-0304335.
 PF
 XX 19-MAY-2000; 2000GB-0012248.
 PR
 XX 23-MAR-2001; 2001GB-0007394.
 XX

PA (PFI2) PFIZER LTD.
 PA (PFI2) PFIZER INC.
 XX
 XX Lewis ME, Robas NM;
 XX
 DR MPI: 2002-306187/35.
 DR N-PSDB: ABK48871.

PT An isolated polynucleotide (I) encoding a G-protein coupled receptor is
 useful in treating disorders e.g. diabetes -
 XX
 XX
 PS Claim 22: Fig 2; 50pp: English.

CC The present invention relates to the isolation of a novel human
 CC G-protein coupled receptor (GPCR), PFI-018, and the polynucleotide
 CC sequence encoding it. Therapeutically the polynucleotide encoding
 CC PFI-018 may be useful in treating obesity, diabetes, metabolic diseases,
 CC neurological diseases, psychotherapeutics, urogenital diseases,
 CC reproductive and sexual diseases, inflammations, cancers, tissue repair,
 CC dermatology, skin pigmentation, photosaging, frailty, osteoporosis,
 CC cardiovascular disease, gastrointestinal disease, infections, allergies,
 CC respiratory disease, sensory organ disorders, sleep disorders and hair
 CC loss. The present sequence represents human GPCR, PFI-018.
 XX

SO Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 23; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSTIGRPOTPGPSTASGVPEVGLRDVASEVALFFMLDLDTAVAGN 60
 DB 1 MESSPIPOSSGNSTIGRPOTPGPSTASGVPEVGLRDVASEVALFFMLDLDTAVAGN 60
 QY 61 AAMVAVIATKPAIRKFFVFHCLVLDLALATMPLAMLSSSLFPHALGGEVACRLYLF 120
 DB 61 AAMVAVIATKPAIRKFFVFHCLVLDLALATMPLAMLSSSLFPHALGGEVACRLYLF 120
 QY 121 LSVCFVSLAIVSAINVERVYVHPMYREVMTLGLVASVLGVWVKALAMASVPVLG 180
 DB 121 LSVCFVSLAIVSAINVERVYVHPMYREVMTLGLVASVLGVWVKALAMASVPVLG 180
 QY 121 LSVCFVSLAIVSAINVERVYVHPMYREVMTLGLVASVLGVWVKALAMASVPVLG 180
 DB 121 LSVCFVSLAIVSAINVERVYVHPMYREVMTLGLVASVLGVWVKALAMASVPVLG 180
 QY 181 RVSMEGASVPPGCSLQNSHSAVCOLFVYVAVLYFLPLLLILVYCGMFVARYAAM 240
 DB 181 RVSMEGASVPPGCSLQNSHSAVCOLFVYVAVLYFLPLLLILVYCGMFVARYAAM 240
 QY 241 OHGPLTWTMETPQORSESLSSRSTMTSSGAPOTPHRTFGGKAHVLLAVGGQFLCW 300
 DB 241 OHGPLTWTMETPQORSESLSSRSTMTSSGAPOTPHRTFGGKAHVLLAVGGQFLCW 300
 QY 301 LPEFSFHLVALSAQISTGVESVVTWIGYFCFTSNPEFGCLNROIIGELSKQFVCFP 360
 DB 301 LPEFSFHLVALSAQISTGVESVVTWIGYFCFTSNPEFGCLNROIIGELSKQFVCFP 360
 QY 361 KPAEELRLPSEGSIEENFILOFGTCPSSESWSRPLPSKQEPNAVDFRIPOQIAE 420
 DB 361 KPAEELRLPSEGSIEENFILOFGTCPSSESWSRPLPSKQEPNAVDFRIPOQIAE 420

DB 361 KPAEELRLPSEGSIEENFILOFGTCPSSESWSRPLPSKQEPNAVDFRIPOQIAE 420
 QY 421 ETSEFLEOOLTSIDISDSYLPRAPASPRLES 451
 DB 421 ETSEFLEOOLTSIDISDSYLPRAPASPRLES 451

RESULT 8
 AAM50637
 ID AAM50637 standard; protein; 451 AA.
 XX
 AC AAM50637;
 XX
 DT 04-APR-2002 (first entry)
 XX

DE Human G protein coupled receptor IGPCR27.

KW IGPCR27; G-protein coupled receptor; receptor; human;
 KW Tourette syndrome; Parkinson's disease; Huntington's disease;
 KW tic; spasm; tremor; dyskinesia; dystonia; pain; analgesic;
 KW neuroleptic; tranquilizer; antiparkinsonian; neuroprotective;
 KW neurotropic; anticonvulsant; metabolic; anorectic; anabolic;
 KW antinflammatory; antidiarrhetic; osteopathic; antibacterial;
 KW fungicide; protozoacide; vitucide; antiaslthmatic; antiallergic;
 KW antithrptic; immunosuppressive; nephroretropic; diagnosis;
 KW central nervous system; therapy.
 KW
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 44..66
 FT /label= Transmembrane_domain-1
 FT Domain 78..98
 FT /label= Transmembrane_domain-2
 FT Domain 116..137
 FT /label= Transmembrane_domain-3
 FT Domain 160..177
 FT /label= Transmembrane_domain-4
 FT Domain 210..230
 FT /label= Transmembrane_domain-5
 FT Domain 291..309
 FT /label= Transmembrane_domain-6
 FT Domain 324..346
 FT /label= Transmembrane_domain-7
 PN MO200202600-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP07534.
 XX
 XX 30-JUN-2000; 2000US-215881P.
 XX
 PA (INGE-) INGENITUM PHARM AG.
 PA
 PI
 PI Wattler F, Wattler S, Trommler P, Nehls MC;
 DR MPI: 2002-140081/18.
 DR N-PSDB: ABA91237.

PT New human or mouse G protein-coupled receptor protein, IGPCR27, useful
 PT for diagnosis, prevention, amelioration or treatment of central nervous
 PT system disorders such as Tourette's syndrome, Parkinson's disease and
 PT pain -
 XX
 XX
 PS Claim 8: Fig 2; 71pp: English.

CC The present sequence is that of human IGPCR27, a novel G protein
 CC coupled receptor expressed exclusively in the brain. The invention
 CC provides human and mouse IGPCR27 polynucleotides and polypeptides,
 CC vectors, host cell expression systems, and transgenic and knockout
 CC animals. Vectors and host cells are used in gene therapy for
 CC prevention, amelioration or treatment of diseases characterized by

CC aberrant expression or activity of IGF2R, where the disease is
 CC associated with signal processing in the central nervous system (CNS)
 CC such as movement dysfunctions, disorders or diseases, tics/tremor,
 CC Tourette's syndrome, Parkinson's disease, Huntington's disease,
 CC dyskinesias, dystonia, pain and spasms (claimed). Knockout,
 CC mutated and transgenic animals are useful for the dissection of the
 CC molecular mechanisms of the IGF2R pathway, for the identification
 CC and cloning of genes able to modify, reduce or inhibit the phenotype
 CC associated with IGF2R activity or deficiency, for the
 CC identification of gene and protein diagnostic markers for diseases,
 CC and for the identification and testing of compounds useful in the
 CC prevention, amelioration or treatment of diseases associated with
 CC IGF2R activity or deficiency (claimed). IGF2R proteins,
 CC nucleic acids, antibodies, agonists and antagonists are useful for
 CC the diagnosis and treatment of CNS disorders, for the detection of
 CC mutant forms of IGF2R or inappropriately expressed forms of
 CC IGF2R, and for drug screening. IGF2R protein is useful in
 CC diagnosis, prevention, amelioration or treatment of diseases
 CC associated with signal processing in CNS, schizophrenia, episodic
 CC paroxysmal anxiety (EPA) disorders such as obsessive compulsive
 CC disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia,
 CC anorexia, kidney diseases such as renal failure, obesity,
 CC gastrointestinal disorders such as irritable bowel syndrome (IBS),
 CC diarrhoea, motility disorders and conditions of delayed gastric
 CC emptying, osteoporosis, infections such as bacterial, fungal,
 CC protozoal and viral infections, asthma, allergy, arthritis,
 CC sepsis and gynaecological disorders. The proteins and nucleic
 CC acids are useful for the identification of compounds effective in
 CC the treatment of disorders based on the aberrant expression or
 CC activity of IGF2R. IGF2R is also useful for the generation of
 CC antibodies, in identification of other cellular gene products
 CC involved in regulating IGF2R, and as a pharmaceutical reagent.

XX
 XX Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 23; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPIPOSSGNSSTIGRVPOTPEPSTASGVPEYGLRDVAESVAFEMLLDLTAVAGN 60
 DB 1 MESSPIPOSSGNSSTIGRVPOTPEPSTASGVPEYGLRDVAESVAFEMLLDLTAVAGN 60
 QY 61 AAVAVIAKTPALKRFVFNLCVLDLALTLTLMPLAMSSALFDHALGEGVACRLYLE 120
 DB 61 AAVAVIAKTPALKRFVFNLCVLDLALTLTLMPLAMSSALFDHALGEGVACRLYLE 120
 QY 121 LSYCFVSLALSYSAINVERYYVHHPRYEVMTGLVASVLCGVWVKALAMASVPLG 180
 DB 121 LSYCFVSLALSYSAINVERYYVHHPRYEVMTGLVASVLCGVWVKALAMASVPLG 180
 QY 181 RVSMEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLDLLLVYCSMFRVARVAM 240
 DB 181 RVSMEGAPSVPPGCSLQMSHSAVCQLFVVFAVLYFLDLLLVYCSMFRVARVAM 240
 QY 241 QHGPLPTWMTPEORBSFSLSRSMWTSAGAPOTPHRTFGGGAAYVLLAVGQFLCW 300
 DB 241 QHGPLPTWMTPEORBSFSLSRSMWTSAGAPOTPHRTFGGGAAYVLLAVGQFLCW 300
 QY 301 LPTFSFHLVVALSAOPISITQGVESVWVWIGYFCTSNPFYGCILNRIIRGELSKQFCF 360
 DB 301 LPTFSFHLVVALSAOPISITQGVESVWVWIGYFCTSNPFYGCILNRIIRGELSKQFCF 360
 QY 361 KPAPBEELRLPREGSIEENFLQFLOGTGPSESWSRPLPSKQEPAPVDFRIQIAE 420
 DB 361 KPAPBEELRLPREGSIEENFLQFLOGTGPSESWSRPLPSKQEPAPVDFRIQIAE 420
 QY 421 ETSEPLEOQLTSDITMSDYLTPASPRLES 451
 DB 421 ETSEPLEOQLTSDITMSDYLTPASPRLES 451

RESULT 9

AA014014
 ID AA014014 standard; Protein; 451 AA.
 AC AA014014;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE Human G protein-coupled receptor Con-218.
 XX
 KW Con-218; G protein-coupled receptor; GPCR; anti-HIV; antiparkinsonian;
 KW neuroprotective; cytosolic; tranquilizer; neuroleptic; antianemic;
 KW antidepressant; immunosuppressive; antimigraine; neuroleptic; antianemic;
 KW antiarteriosclerotic; antidiabetic; thrombolytic; antipsoriatic;
 KW vasotropic; anticonvulsant; antithyroid; antiinflammatory; nephrotoxic;
 KW hypotensive; antineumatic; antiarthritic; cerebroprotective; vitruclide;
 KW antifertility; gene therapy; thyroid disorder; renal failure;
 KW inflammatory conditions; cell differentiation; homeostasis; CNS disorder;
 KW rheumatoid arthritis; autoimmune disorder; movement disorder; stroke;
 KW psychotic disorder; neurological disorder; dyskinesia; infection;
 KW attention disorder; degenerative disorder; metabolic; cardiovascular;
 KW cancer; hyperproliferative disorder; psoriasis; hormonal disorder;
 KW sexual dysfunction; schizophrenia; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 44..66 /label= Transmembrane_domain
 FT Domain 77..99 /label= Transmembrane_domain
 FT Domain 118..136 /label= Transmembrane_domain
 FT Domain 156..178 /label= Transmembrane_domain
 FT Domain 207..229 /label= Transmembrane_domain
 FT Domain 285..307 /label= Transmembrane_domain
 FT Domain 326..344 /label= Transmembrane_domain
 FT Domain /label= Transmembrane_domain
 PN WO200181576-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 19-APR-2001; 2001WO-US12690.
 XX
 PR 19-APR-2000; 2000US-198600P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Lind P, Berthold M;
 XX
 DR WPI; 2002-041403/05.
 DR N-PSDB; AAK98269.
 XX
 PT Novel gene encoding G protein-coupled receptor termed Con-218, useful
 PT for identifying compounds that are useful for treating inflammatory
 PT conditions, central nervous system disorders and cardiovascular
 PT disorders -
 PS Claim 31; Page 73; 126pp; English.
 XX
 XX The sequence represents Con-218, the novel human G protein-coupled
 CC receptor (GPCR) of the invention. The polypeptide of the invention has
 CC anti-HIV, antiparkinsonian, neuroprotective, cytosolic, tranquilizer,
 CC neuroleptic, antianemic, antidepressant, immunosuppressive, antimigraine,
 CC vasotropic, antiarteriosclerotic, cardiant, antidiabetic, thrombolytic,
 CC antipsoriatic, vasotropic, anticonvulsant, antithyroid, antiinflammatory,
 CC nephrotoxic, hypotensive, antineumatic, antiarthritic,
 CC cerebroprotective, antifertility, and vitruclide activity. The Con-218
 CC works as a modulator of neuropeptide binding or signalling, in a vaccine
 CC or gene therapy. The polypeptide and polynucleotide are useful for the

CC treatment of thyroid disorders; renal failure; inflammatory conditions;
 CC cell differentiation and homeostasis diseases; rheumatoid arthritis;
 CC autoimmune disorders; movement disorders; CNS disorders; stroke;
 CC psychotic and neurological disorders; dyskinesias; attention disorders;
 CC degenerative disorders; infections; metabolic and cardiovascular
 CC diseases and disorders; proliferative diseases and cancers;
 CC hyperproliferative disorders; psoriasis; hormonal disorders; and sexual
 CC dysfunction. The polypeptide is also useful for inducing an immune
 CC response in a mammal against itself, and for identifying a compound that
 CC binds Con-281. Con-218 molecules are useful for identifying a compound
 CC which modulates the activity of Con-218 polypeptides. The polypeptide is
 CC also useful for identifying compounds useful for the treatment of
 CC schizophrenia. Furthermore, the polypeptide is useful for purifying a G
 CC protein from a sample containing G-protein.

SO Sequence 451 AA:

Query Match 100.0%; Score 2318; DB 23; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MESSPIPOSSGSSSTIGRVPTGPGPTASGVPVGLRDVASESVAFEMLLDLTAAGN 60
 DB 1 MESSPIPOSSGSSSTIGRVPTGPGPTASGVPVGLRDVASESVAFEMLLDLTAAGN 60

OY 61 AAVMAVIATKTPALRKFFVFHNLCLVDLLAALTMLPLAMSSSALFDHALGEGVACRLYLE 120
 DB 61 AAVMAVIATKTPALRKFFVFHNLCLVDLLAALTMLPLAMSSSALFDHALGEGVACRLYLE 120

OY 121 LSYCFVSLATLSVSAINVERYYVHPMRYEVRMTGLVASVLGVWVKALMAASVPVLG 180
 DB 121 LSYCFVSLATLSVSAINVERYYVHPMRYEVRMTGLVASVLGVWVKALMAASVPVLG 180

OY 181 RVSMEGAPSVPPGCSIQMWSHSAVCQLFVVVFVFLVFLPLLILVYVCSMPFARVAAAM 240
 DB 181 RVSMEGAPSVPPGCSIQMWSHSAVCQLFVVVFVFLVFLPLLILVYVCSMPFARVAAAM 240

OY 241 QHGRLPTWMTTPRQRESLSRSTMTWSSGAPQTPHRTFGGKAAVLLAVGGQFLLCW 300
 DB 241 QHGRLPTWMTTPRQRESLSRSTMTWSSGAPQTPHRTFGGKAAVLLAVGGQFLLCW 300

OY 301 LPIFSFHLVVALSAOPISTGQVESVVTWIGYFCFTSNPFYGCGLNROIKELSKQFVCF 360
 DB 301 LPIFSFHLVVALSAOPISTGQVESVVTWIGYFCFTSNPFYGCGLNROIKELSKQFVCF 360

OY 361 KPAPEELRLPRREGSIEENFLQFLOCTGCPSESWSRPLPSPKQEPADVDFRIPOIAE 420
 DB 361 KPAPEELRLPRREGSIEENFLQFLOCTGCPSESWSRPLPSPKQEPADVDFRIPOIAE 420

OY 421 ETSEPLEQQLTSDIIMSDSYLRPAASPRLES 451
 DB 421 ETSEPLEQQLTSDIIMSDSYLRPAASPRLES 451

RESULT 10
 AAU74909 standard: Protein; 451 AA.
 XX AAU74909;
 XX 09-APR-2002 (first entry)
 DE Amino acid sequence of human G-protein coupled receptor TGR213 protein.
 XX Human: G-protein coupled; receptor; GPCR; TGR213; kidney disease;
 KW signal transduction modulator; cerebral cavernous malformation;
 KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;
 KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;
 KW spleen-associated disorder; immune disorder.
 XX Homo sapiens.
 OS
 XX MO200200719-A2.

XX 03-JAN-2002.
 PD 25-JUN-2001: 2001MO-US20363.
 PF 23-JUN-2000: 2000US-213461P.
 XX (TULU-) TULARIK INC.
 PA Lin DC, Zhao J, Chen J, Cutler G;
 XX WPI, 2002-147880/19.
 DR N-PSDB: ABR12962.
 XX New G-protein coupled receptor polypeptides, useful for identifying
 PT modulators of signal transduction for treating kidney disease,
 PT hyperlipidemia, obesity, dyslexia and cardiac myxoma -
 XX Claim 26; Page 65; 78pp; English.

CC The present invention relates to a new G-protein coupled receptor (GPCR)
 CC polypeptide comprising greater than 70% amino acid sequence identity to
 CC the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2,
 CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18
 CC or 90% amino acid sequence identity to human novel edg receptor protein,
 CC as defined in the specification. The GPCR covalently linked to a solid
 CC phase is useful for identifying a compound that modulates signal
 CC transduction. The identified compounds are useful for treating
 CC kidney disease, cerebral cavernous malformations, hyperlipidemia,
 CC obesity, dyslexia and cardiac myxoma. The molecules of the invention are
 CC useful for diagnosing disorders or conditions such as kidney-related
 CC conditions or diseases such as renal failure, nephritis, nephrotic
 CC syndrome, asymptomatic urinary abnormalities, renal tubule defects,
 CC hypertension and nephrolithiasis, liver-related disease or condition
 CC e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice
 CC and spleen-associated disorders or conditions e.g. splenic enlargement,
 CC immune disorders, blood disorders and others. Modulation of the
 CC polypeptide of the invention is useful to treat or prevent any of the
 CC above conditions or diseases. The present amino acid sequence represents
 CC the human GPCR TGR213 protein of the invention. This sequence is one of
 CC seven novel G protein coupled receptors of the invention (AAU74904-
 CC AAU74911).

Query Match 100.0%; Score 2318; DB 23; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MESSPIPOSSGSSSTIGRVPTGPGPTASGVPVGLRDVASESVAFEMLLDLTAAGN 60
 DB 1 MESSPIPOSSGSSSTIGRVPTGPGPTASGVPVGLRDVASESVAFEMLLDLTAAGN 60

OY 61 AAVMAVIATKTPALRKFFVFHNLCLVDLLAALTMLPLAMSSSALFDHALGEGVACRLYLE 120
 DB 61 AAVMAVIATKTPALRKFFVFHNLCLVDLLAALTMLPLAMSSSALFDHALGEGVACRLYLE 120

OY 121 LSYCFVSLATLSVSAINVERYYVHPMRYEVRMTGLVASVLGVWVKALMAASVPVLG 180
 DB 121 LSYCFVSLATLSVSAINVERYYVHPMRYEVRMTGLVASVLGVWVKALMAASVPVLG 180

OY 181 RVSMEGAPSVPPGCSIQMWSHSAVCQLFVVVFVFLVFLPLLILVYVCSMPFARVAAAM 240
 DB 181 RVSMEGAPSVPPGCSIQMWSHSAVCQLFVVVFVFLVFLPLLILVYVCSMPFARVAAAM 240

OY 241 QHGRLPTWMTTPRQRESLSRSTMTWSSGAPQTPHRTFGGKAAVLLAVGGQFLLCW 300
 DB 241 QHGRLPTWMTTPRQRESLSRSTMTWSSGAPQTPHRTFGGKAAVLLAVGGQFLLCW 300

OY 301 LPIFSFHLVVALSAOPISTGQVESVVTWIGYFCFTSNPFYGCGLNROIKELSKQFVCF 360
 DB 301 LPIFSFHLVVALSAOPISTGQVESVVTWIGYFCFTSNPFYGCGLNROIKELSKQFVCF 360

QY 361 KPAEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKPOEPPAVDFRIPQIAE 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 KPAEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKPOEPPAVDFRIPQIAE 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 ETSEFLQQLTSDITMSDYLRPAASPRLES 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 ETSEFLQQLTSDITMSDYLRPAASPRLES 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 11
 AAU11895
 ID AAU11895 standard; Protein: 451 AA.
 XX AAU11895;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX
 DE Human novel G protein-coupled receptor, GPCR8a.
 XX
 XX Human: GPCR8a; G protein coupled receptor; developmental disease;
 KM Immune disease; taste and scent detectability disorder;
 KM Burkitt's lymphoma; signal transduction pathway disorder;
 KM retinal disease; cell growth rate disorder; feeding disorder;
 KM control of feeding; obesity; starvation; fungal infection;
 KM noninsulin-dependent diabetes mellitus; bacterial infection;
 KM protozoal infection; viral infection; pain; cancer; anorexia; bulimia;
 KM asthma; Parkinson's disease; acute heart failure; hypotension;
 KM hypertension; urinary retention; osteoporosis; Crohn's disease;
 KM multiple sclerosis; Albright Hereditary Osteodystrophy; angina pectoris;
 KM myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
 KM manic depression; delirium; dementia; severe mental retardation;
 KM autosomal dominant (2) Acrocallosal syndrome; dyskinesia;
 KM Huntington's disease; Gilles de la Tourette syndrome; haematopoietic disorder; cell signal processing disorder;
 KM metabolic pathway modulation disorder.
 KM
 XX Homo sapiens.
 OS
 XX
 PN WO200190187-A2.
 PD
 XX 29-NOV-2001.
 PF
 XX 24-MAY-2001; 2001WO-US17114.
 PR 24-MAY-2000; 2000US-206757P.
 PR 25-MAY-2000; 2000US-207020P.
 PR 28-JUN-2000; 2000US-214372P.
 PR 19-JUL-2000; 2000US-219786P.
 PR 25-JUL-2000; 2000US-220593P.
 PR 10-OCT-2000; 2000US-239542P.
 PR 18-DEC-2000; 2000US-256402P.
 PR 26-FEB-2001; 2001US-271645P.
 PR 09-MAR-2001; 2001US-274809P.
 PR 13-MAR-2001; 2001US-275590P.
 XX
 XX (CURAGEN CORP.
 PA
 XX Padigaru M, Spytek KA, Majumder K, Tchernev VM, Grosse WM;
 PI Szefereres ED, Alsobrook JP, Burgess CE, Shimkets RA, Taupier RJ;
 PI Casman SJ, Gangoli E, MacDougall JR, Stone DJ, Smithson G;
 XX
 DR WPI: 2002-106188/14.
 DR N-PDB: AAS19412.
 XX
 XX New polypeptide, useful for treating pain, cancer, urinary retention,
 PT osteoporosis, Crohn's disease, dyskinesias, acute heart failure,
 PT dementia, asthma and ulcer, comprises the isolated G-coupled
 PT protein-receptor GPCR8 -
 XX
 PS Claim 1; Page 35; 154pp; English.
 XX
 CC The invention relates to an isolated G protein-coupled receptor related
 CC polypeptide (GPCR1a, 1b, 2, 3a, 3b, 4, 5, 6a, 6b, 7, 8a, 8b, and GPCR9)

CC and the polynucleotides encoding them. The GPCR, its encoding
 CC polynucleotide and an anti-GPCR antibody are useful for diagnosing
 CC treating or preventing a GPCR-associated disorder in a human e.g.
 CC developmental diseases, immune diseases, taste and scent detectability
 CC disorder, Burkitt's lymphoma, signal transduction pathway disorders,
 CC retinal diseases including those involving photoreception, cell growth
 CC rate disorders, feeding disorders, control of feeding, potential
 CC obesity due to over-eating, potential disorders due to starvation,
 CC noninsulin-dependent diabetes mellitus, bacterial, fungal, protozoal
 CC and viral infections, pain, cancer, anorexia, bulimia, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
 CC Albright Hereditary Osteodystrophy, angina pectoris, myocardial
 CC infarction, delirium, allergies, benign prostatic hypertrophy, manic
 CC depression, delirium, dementia, severe mental retardation, autosomal
 CC dominant (2) Acrocallosal syndrome and dyskinesias, such as
 CC Huntington's disease or Gilles de la Tourette syndrome, haematopoietic
 CC disorders, and disorders related to cell signal processing and
 CC metabolic pathway modulation. The present sequence represents GPCR8a.
 XX
 SQ Sequence 451 AA:
 Query Match 100.0%; Score 2318; DB 23; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2,4e-228;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MESSPIQSSNSTLRVOTPEPSTASGYPEGLDVAASEVALFPMILLDTITAVAGN 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MESSPIQSSNSTLRVOTPEPSTASGYPEGLDVAASEVALFPMILLDTITAVAGN 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 AAVAVAIAKPAALAKFFVFPHLCVDDLALTLPLMLSSALFDHAFGEVACRLYLF 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 AAVAVAIAKPAALAKFFVFPHLCVDDLALTLPLMLSSALFDHAFGEVACRLYLF 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 LSVCFVSLALISVAIINVERYYVHPMRYEVRMTGLVASVLGVWVKALAMASVPVLG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 LSVCFVSLALISVAIINVERYYVHPMRYEVRMTGLVASVLGVWVKALAMASVPVLG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 RVSMEEGAPSVPGCSLQMSHSAVCQLEVVFAVLYFLPLLLLVYCSFRRARVAM 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 RVSMEEGAPSVPGCSLQMSHSAVCQLEVVFAVLYFLPLLLLVYCSFRRARVAM 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 QHGPLPTWMEETPROSESLSSRTMTWSSGAPQTTPTRTGCGAAVLLAVGQFLICW 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 QHGPLPTWMEETPROSESLSSRTMTWSSGAPQTTPTRTGCGAAVLLAVGQFLICW 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 LPYFPHLYVALSAQPISTGVESVWVWIGYCFPTSNPFYGCILNROIIGELSKQVCF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 LPYFPHLYVALSAQPISTGVESVWVWIGYCFPTSNPFYGCILNROIIGELSKQVCF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 KPAEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKPOEPPAVDFRIPQIAE 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 KPAEEELRLPREGSIEENFLQGTGCPSESWSRPLPSKPOEPPAVDFRIPQIAE 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 ETSEFLQQLTSDITMSDYLRPAASPRLES 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 ETSEFLQQLTSDITMSDYLRPAASPRLES 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 12
 AAU17073
 ID AAU17073 standard; Protein: 451 AA.
 XX
 XX AAU17073;
 AC
 XX 18-APR-2002 (first entry)
 DT
 XX
 DE Human G-protein coupled receptor (GPCR2) protein.
 XX
 XX Human: G-protein coupled receptor; GPCR2; cerebroprotective; vomiting;
 KM receptor-mediated disorder; therapy; urinary retention; allergy; obesity;
 KM osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;
 KM anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;

KW		stroke;hypertension; neuronal disorder; neurodegenerative disease; antibacterial;
KM		depression; mental retardation; dementia; ischemia; Parkinson's disease; Alzheimer's diseases; demantla; Ischaemia; Parkinson's disease; antiviral;
KM		Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;
KV		vulnerarity; analgesic; anorectic; anabolic; diuretic; cardiact; nootropic;
XK		antiemetic; vasotrophic; diabetes; cancer; tranquilizer; neuroleptic.
XX		
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	DomaIn	45..68 /note- "Transmembrane domain"
FT	DomaIn	78..99 /note- "transmembrane domain"
FT	DomaIn	117..138 /note- "Transmembrane domain"
FT	DomaIn	154..179 /note- "transmembrane domain"
FT	DomaIn	207..228 /note- "transmembrane domain"
FT	DomaIn	287..305 /notes- "transmembrane domain"
FT	DomaIn	325..344 /note- "transmembrane domaIn"
PX		
NN	MO200198330-A2.	
XX		
PD	27-Dec-2001.	
PF	20-JUN-2001; 2001WO-BE00104.	
XX		
PR	20-JUN-2000; 2000US-212913P.	
PR	11-JUL-2000; 2000US-217494P.	
PR	26-JAN-2001; 2001EP-0870015.	
PR	12-FEB-2001; 2001EP-0870024.	
XA	(EURO-) EUROSCREEN SA.	
PA		
PI	Lanroy V, Brezillon S, Dethoux M, Parmentier M, Govarts C;	
DR	WPt: 2002-130789/17.	
N-PsDB:	AAD27493.	
PT	New G-protein coupled receptor, useful in the manufacture of	
PT	medaments for treating receptor mediated disorders e.g. acute heart	
XX	failure and Alzheimer's disease -	
PS	Disclosure: Page 21; 46pp; English.	
CC	The present invention relates to a G-protein couplred receptor (GPCR) and	
CC	nucleotide encoding it. GPCR are useful in the manufacture of a	
CC	medicament for the prevention and/or treatment of receptor-mediated	
CC	disorders e.g. viral infections, virus and bacterial diseases, diseases	
CC	and disorders involving disturbances of cell migration, diseases or	
CC	perturbations of immune system including cancers, development of tumours	
CC	and tumour metastasis, inflammatory and neoplastic processes; Bacterial	
CC	and fungal infections, In wound and bone healing, dysfunction of	
CC	regulatory growth functions; pains, diabetes, obesity, anorexia, bulimia,	
CC	urinary retention, osteoporosis, angina pectoris, arteriosclerosis,	
CC	restenosis, diseases involving excessive or reduced proliferation or loss	
CC	of smooth muscle cells, aneurysm, stroke, ischæmia, ulcers, allergies,	
CC	bénign prostatic hypertrophy, migraine, vomiting; blood circulating	
CC	affectiors including acute heart failure, hypotension, hypertension and	
CC	myocardial infarction psychotic; neuronal disorders such as anxiety,	
CC	sclizophrenia, manic depression, depression, delirium, dementia, severe	
CC	mental retardation; degenerative diseases; neurodegenerative diseases	
CC	such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g.	
CC	Huntington's disease or Gilles de la Tourette's syndrome and other	
CC	related diseases. The present sequence is GPcRx2 protein.	
QO	Sequence 451 AA;	

```

Query Match      100.08;  Score 2318;  DB 23;  Length 451;

```

```
Best Local Similarity 100.0%; Pred. No. 2.4e-228;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	MESSITPOSSGNSSTLGRVPTPOGPSTASGVPYGLRDAVASEVALPFMLLDLTRVACN	60
Db	1	MESSITPOSSGNSSTLGRVPTPOGPSTASGVPYGLRDAVASEVALPFMLLDLTRVACN	60
QY	61	AAVMAVIAKTPALRKRFVVFHILCLVYDLAAITLMPPLAMLSSSALPDBALFGEVACRLYLF	120
Db	61	AAVMAVIAKTPALRKRFVVFHILCLVYDLAAITLMPPLAMLSSSALPDBALFGEVACRLYLF	120
QY	121	LSVCFVSLATLVSAINVERYVYVHPMRYEVRMTGLVASVLGVWAKALAMASVPVLG	180
Db	121	LSVCFVSLATLVSAINVERYVYVHPMRYEVRMTGLVASVLGVWAKALAMASVPVLG	180
QY	181	RYSMEGASVPYPCGSLQMSHSAQCOLFVYVFAVLYPLLLLLILVYCSMPFVAVAAVM	240
Db	181	RYSMEGASVPYPCGSLQMSHSAQCOLFVYVFAVLYPLLLLLILVYCSMPFVAVAAVM	240
QY	241	QHGPLPTMETPRORSESLSSRSRTMVSSSGAPQYTPHRTFGGGKAHVLLAVAGGQFLCM	300
Db	241	QHGPLPTMETPRORSESLSSRSRTMVSSSGAPQYTPHRTFGGGKAHVLLAVAGGQFLCM	300
QY	301	LPYSFHLIYVALSNQPISTGQVESVYMWIGYFCTSNPFYGGCLNQINGELSKQVCFE	360
Db	301	LPYSFHLIYVALSNQPISTGQVESVYMWIGYFCTSNPFYGGCLNQINGELSKQVCFE	360
QY	361	KPAPEELRLRSRGSIIEENFLQGLQGTGCPSESWSRPLPSRKQBPAPVADRIFPOIAE	420
Db	361	KPAPEELRLRSRGSIIEENFLQGLQGTGCPSESWSRPLPSRKQBPAPVADRIFPOIAE	420
QY	421	ETSEFLQOQLTSDIIMSDSYLRPAASRLRS	451
Db	421	ETSEFLQOQLTSDIIMSDSYLRPAASRLRS	451

RESULT 13	
ABB05445	
ID	ABB05445 standard; Protein; 451 AA.
XX	
AC	ABB05445;
XX	
DT	16-APR-2002 (first entry)
XX	
DE	Human G-protein coupled receptor GPRM412 protein SEQ ID NO:2.
XX	
FN	Human G-protein coupled receptor; GPRM412; receptor; antibacterial;
XX	fungicide; protozoocide; virucide; anti-HIV; analgesic; cytostatic; pain
XX	antidiabetic; anorectic; antiasthmatic; antiparkinsonian; caditant;
XX	hypertensive; hypotensive; osteopathic; antianginal; cerebroprotective;
XX	antifurcer; antiallergic; antimigraine; antiemetic; tranquilizer; cancer
XX	neuroleptic; antineoplastic; antidepressant; anticonvulsant; nootropic; ulcer
XX	vaccine; gene; infection; diabetes; obesity; anorexia; bulimia; asthma;
XX	Parkinson's disease; acute heart failure; hypotension; hypertension;
XX	urinary retention; osteoporosis; angina pectoris; stroke; schizophrenia;
XX	myocardial infarction; allergy; benign prostatic hypertrophy; migraine;
XX	vomiting; psychotic; neurological disorder; anxiety; manic depression;
XX	depression; delirium; dementia; severe mental retardation; dyskinesia;
XX	Huntington's disease; Gilles de la Tourette's syndrome.
OS	Homo sapiens.
XX	
PN	WO200198490-A1.
XX	
PD	27-DEC-2001.
XX	
PF	15-JUN-2001; 2001WO-EP06729.
XX	
PR	21-JUN-2000; 2000EP-0113239.
XX	
PA	(MERE) MERCK PATENT GMBH.
XX	
PI	Kluxen F, Duecker K;

XX WPI; 2002-139788/18.
DR N-PSDB; ABA93134.
XX
PT Novel G-protein coupled receptor polypeptides and polynucleotides
PT useful in screening assays and for treating diabetes, cancer,
PT osteoporosis, asthma, neurological disorders and identifying modulators
PT useful in therapy -
XX
XX
PS Claim 1; Page 40-41; 44pp: English.
XX
XX The present sequence represents a human G-protein coupled receptor
CC designated GPRM42 (1). (1) has antibacterial, fungicidal, protozoacidal,
CC virucidal, anti-HIV, analgesic, cytostatic, antidiabetic, anorectic,
CC antisthmatic, antiparkinsonian, cardiant, hypertensive, hypotensive,
CC osteopathic, antianginal, cerebroprotective, antitumor, antiallergic,
CC antitubercular, antileptic, tranquilizer, neuroleptic, antidepressant,
CC antitumor, anticonvulsant and neurotropic activities, and it can be used
CC in vaccine production. (1) can be used in screening assays to identify
CC compounds that stimulate or inhibit the function or level of (1). (1)
CC and the polynucleotide (1) encoding it can be used in treating and
CC preventing human diseases including infections, particularly infections
CC caused by HIV-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,
CC bulimia, asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris, stroke,
CC myocardial infarction, ulcer, allergy, benign prostatic hypertrophy,
CC migraine, vomiting, psychotic and neurological disorders, including
CC anxiety, schizophrenia, manic depression, depression, delirium, dementia,
CC severe mental retardation, dyskinesias such as Huntington's disease or
CC Gilles de la Tourette's syndrome.
XX
XX
SQ Sequence 451 AA:
Query Match 100.0%; Score 2318; DB 23; Length 451;
Best Local Similarity 100.0%; Pred. No. 2,4e-228;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60
XX
QY 61 AAVMAVIATKTPALRKFEVFEHCLVDLALTLMTPLAMLSLALFDHALGEGVACRLYLE 120
Db 61 AAVMAVIATKTPALRKFEVFEHCLVDLALTLMTPLAMLSLALFDHALGEGVACRLYLE 120
XX
QY 121 LSYCFVSLALISYAINVERYYVYVHPMRYEVRMTGLVASVLGVWVKALAMASVPVLG 180
Db 121 LSYCFVSLALISYAINVERYYVYVHPMRYEVRMTGLVASVLGVWVKALAMASVPVLG 180
XX
QY 181 RVSMEGAPSVPPGCSLQMSHSAVYVFAVLVFLPLLLILVYVCMFVARARAA 240
Db 181 RVSMEGAPSVPPGCSLQMSHSAVYVFAVLVFLPLLLILVYVCMFVARARAA 240
XX
QY 241 QHGPPLPTMTPTPORSSELSRSTWYTSAGAPQTPHRTFGGKAQVLLAVGQFLICW 300
Db 241 QHGPPLPTMTPTPORSSELSRSTWYTSAGAPQTPHRTFGGKAQVLLAVGQFLICW 300
XX
QY 301 LPTFSFLIYALSAQPTSTQVSVYTWIGYFCFTSNPFYGCILNROIKELSKQVCF 360
Db 301 LPTFSFLIYALSAQPTSTQVSVYTWIGYFCFTSNPFYGCILNROIKELSKQVCF 360
XX
QY 361 KRPPEELRLRPSREGSIEENFLOFLOGTGCPSRSWVSRPLSPKQPPAVDFITPGQIAE 420
Db 361 KRPPEELRLRPSREGSIEENFLOFLOGTGCPSRSWVSRPLSPKQPPAVDFITPGQIAE 420
XX
QY 421 ETSEPLEOQLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEPLEOQLTSDIIMSDSYLRPAASPRLES 451
XX
RESULT 14
AAU04386
ID AAU04386 standard; Protein; 869 AA.

XX AC AAU04386;
XX 23-OCT-2001 (first entry)
XX
XX GPCR-Gs fusion protein, hRUP13-GS.
XX
XX G-protein coupled receptor; GPCR; hRUP13-GS; agonist;
XX Inverse agonist; lung cancer.
XX
XX Chimeric - Homo sapiens.
XX Chimeric - Rattus sp.
XX
XX W0200136471-A2.
XX
XX 25-MAY-2001.
XX
XX
XX 16-NOV-2000; 2000MO-US31509.
XX
XX 17-NOV-1999; 99US-0166088.
XX 17-NOV-1999; 99US-0166099.
XX 17-NOV-1999; 99US-0166369.
XX 23-DEC-1999; 99US-0171900.
XX 23-DEC-1999; 99US-0171901.
XX 23-DEC-1999; 99US-0171902.
XX 11-FEB-2000; 2000US-0181749.
XX 14-MAR-2000; 2000US-0189258.
XX 14-MAR-2000; 2000US-0189259.
XX 10-APR-2000; 2000US-0195898.
XX 10-APR-2000; 2000US-0195899.
XX 10-APR-2000; 2000US-0195899.
XX 28-APR-2000; 2000US-0200419.
XX 12-MAY-2000; 2000US-0203630.
XX 12-JUN-2000; 2000US-0210741.
XX 12-JUN-2000; 2000US-0210982.
XX 21-AUG-2000; 2000US-0226760.
XX 26-SEP-2000; 2000US-0235418.
XX 26-SEP-2000; 2000US-0235779.
XX 20-OCT-2000; 2000US-0242332.
XX 20-OCT-2000; 2000US-0242343.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Chen R, Dang HT, Lowitz KP,
XX
XX WPI; 2001-355616/37.
XX N-PSDB; AAS08271.
XX
XX Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents -
XX
XX Example 5; Page 146-149; 160pp: English.
XX
XX The sequence is a G-protein coupled receptor (GPCR) fusion protein,
CC hRUP13-GS, being the human hRUP13 fused to the rat Gs protein.
CC The endogenous and non-endogenous, constitutively activated versions
CC of human G-protein coupled receptors (GPCR), are useful for direct
CC identification of candidate compounds as receptor agonists, inverse
CC agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer.
CC Non-endogenous version of human GPCRs are also utilized in research
CC settings and in vitro and in vivo system, incorporating GPCRs can be
CC utilized to elucidate and understand the roles these receptors
CC play in the human condition, both normal and diseased.
XX
XX
SQ Sequence 869 AA:
Query Match 100.0%; Score 2318; DB 22; Length 869;
Best Local Similarity 100.0%; Pred. No. 6e-228;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESSPIPOSSGNSSTLGRVPTGPSTASGVPEVGLRDVASEVALFFMLLDLTAVAGN 60

|||||
Db 1 MESSPIPOSSGNSSTLGRVQTPGPGSTAGVPEVGLRDVASESVALFPMLLDLTAVAGN 60
Oy 61 AAMVAIAKTPALRKRFVFNHLCVLDLALATLMPALAMSSSLPFDHALGEGVACRLTYLF 120
Db 61 AAMVAIAKTPALRKRFVFNHLCVLDLALATLMPALAMSSSLPFDHALGEGVACRLTYLF 120
Oy 121 LSVCFVSLATLSVSAINVERRYVVHPMRREVMRTGLVASVLGVWVKALAMASVPVLG 180
Db 121 LSVCFVSLATLSVSAINVERRYVVHPMRREVMRTGLVASVLGVWVKALAMASVPVLG 180
Oy 181 RVSMEGASVPVPGCSLQMSHSAVQCLFVVVFALVFLPLLLILVYVCSMPFVARVAA 240
Db 181 RVSMEGASVPVPGCSLQMSHSAVQCLFVVVFALVFLPLLLILVYVCSMPFVARVAA 240
Oy 241 QHGPPLTMMETPRQRESLSRSTMTSSGAPQTPHRTFGGKAHVLLAVGGQFLCW 300
Db 241 QHGPPLTMMETPRQRESLSRSTMTSSGAPQTPHRTFGGKAHVLLAVGGQFLCW 300
Oy 301 LPYFSFHLVVALSAOPISITGQVESVVTWIGFCFTSNPFYGCGLNRQIRGELSKQFVCF 360
Db 301 LPYFSFHLVVALSAOPISITGQVESVVTWIGFCFTSNPFYGCGLNRQIRGELSKQFVCF 360
Oy 361 KPAPEELRLPREGSIEENFLQFLQGTGCPSSSWSRPLPSKQPPAVDFRIPQIAE 420
Db 361 KPAPEELRLPREGSIEENFLQFLQGTGCPSSSWSRPLPSKQPPAVDFRIPQIAE 420
Oy 421 ETSEFLEQOLTSDIIMSDSYLRPAASPRLES 451
Db 421 ETSEFLEQOLTSDIIMSDSYLRPAASPRLES 451
*RESULT 15
AAU11896
ID AAU11896 standard; Protein: 451 AA.
XX
XX AAU11896;
DT 26-MAR-2002 (first entry)
DE Human novel G protein-coupled receptor, GPCR8b.
XX
KW Human; GPCR8b; G protein coupled receptor; developmental disease;
KW Immune disease; taste and scent detectability disorder;
KW Burkitt's lymphoma; signal transduction pathway disorder;
KW retinal disease; cell growth rate disorder; feeding disorder;
KW control of feeding; obesity; starvation; fungal infection;
KW noninsulin-dependent diabetes mellitus; bacterial infection;
KW protozoal infection; viral infection; pain; cancer; anorexia; bulimia;
KW asthma; Parkinson's disease; acute heart failure; hypotension;
KW hypertension; urinary retention; osteoporosis; Crohn's disease;
KW multiple sclerosis; Albritght Hereditary Osteodystrophy; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW manic depression; delirium; dementia; severe metal retardation;
KW autosomal dominant (2) Acrocallosal syndrome; dyskinesia;
KW Huntington's disease; Gilles de la Tourette syndrome;
KW haematopoietic disorder; cell signal processing disorder;
KW metabolic pathway modulation disorder.
OS Homo sapiens.
XX
XX WO200190187-A2.
PN
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US17114.
XX
PR 24-MAY-2000; 2000US-206757P.
PR 25-JUN-2000; 2000US-207020P.
PR 28-JUN-2000; 2000US-214372P.
PR 19-JUL-2000; 2000US-219786P.
PR 25-JUL-2000; 2000US-220593P.
PR 10-OCT-2000; 2000US-239342P.

PR 18-DEC-2000; 2000US-256402P.
PR 26-FEB-2001; 2001US-271645P.
PR 09-MAR-2001; 2001US-274809P.
PR 13-MAR-2001; 2001US-275590P.
XX
PA (CURA-) CUBAGEN CORP.
XX
PI Padigaru M, Spytek KA, Majumder K, Tchernev VT, Grosse WM;
PI Szerkner ED, Alsbrook JP, Burgess CE, Shinkets RA, Taupier RJ;
PI Casman SJ, Gangolli E, MacDougall JR, Stone DJ, Smltson G;
XX
DR WPI; 2002-106188/14.
XX
DR N-PSDB: AAS19413.
XX
PT New polypeptide, useful for treating pain, cancer, urinary retention,
PT osteoporosis, Crohn's disease, dyskinesias, acute heart failure,
PT dementia, asthma and ulcer, comprises the isolated G-coupled
PT protein-receptor GPCR8
XX
PS Claim 1; Page 37; 154pp; English.
XX
CC The invention relates to an isolated G protein-coupled receptor related
CC polypeptide (GPCR1a, 1b, 2, 3a, 3b, 4, 5, 6a, 6b, 7, 8a, 8b, and GPCR9)
CC and the polynucleotides encoding them. The GPCR, its encoding
CC polynucleotide and an anti-GPCR antibody are useful for diagnosing
CC treating or preventing a GPCR-associated disorder in a human e.g.
CC developmental diseases, immune diseases, taste and scent detectability
CC disorder, Burkitt's lymphoma, signal transduction pathway disorders,
CC retinal diseases including those involving photoreception, cell growth
CC rate disorders, feeding disorders, control of feeding, potential
CC obesity due to over-eating, potential disorders due to starvation,
CC noninsulin-dependent diabetes mellitus, bacterial, fungal, protozoal
CC and viral infections, pain, cancer, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
CC Albritght Hereditary Osteodystrophy, angina pectoris, myocardial
CC infarction, ulcers, allergies, benign prostatic hypertrophy, manic
CC depression, delirium, dementia, severe metal retardation, autosomal
CC dominant (2) Acrocallosal syndrome and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette syndrome, haematopoietic
CC disorders, and disorders related to cell signal processing and
CC metabolic pathway modulation. The present sequence represents GPCR8b.
XX
SQ Sequence 451 AA:
Query Match 100.0%; Score 2317; DB 23; Length 451;
Best local Similarity 99.8%; Pred. No. 3, 1e-228;
Matches 450; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MESSPIPOSSGNSSTLGRVQTPGPGSTAGVPEVGLRDVASESVALFPMLLDLTAVAGN 60
Db 1 MESSPIPOSSGNSSTLGRVQTPGPGSTAGVPEVGLRDVASESVALFPMLLDLTAVAGN 60
Oy 61 AAMVAIAKTPALRKRFVFNHLCVLDLALATLMPALAMSSSLPFDHALGEGVACRLTYLF 120
Db 61 AAMVAIAKTPALRKRFVFNHLCVLDLALATLMPALAMSSSLPFDHALGEGVACRLTYLF 120
Oy 121 LSVCFVSLATLSVSAINVERRYVVHPMRREVMRTGLVASVLGVWVKALAMASVPVLG 180
Db 121 LSVCFVSLATLSVSAINVERRYVVHPMRREVMRTGLVASVLGVWVKALAMASVPVLG 180
Oy 181 RVSMEGASVPVPGCSLQMSHSAVQCLFVVVFALVFLPLLLILVYVCSMPFVARVAA 240
Db 181 RVSMEGASVPVPGCSLQMSHSAVQCLFVVVFALVFLPLLLILVYVCSMPFVARVAA 240
Oy 241 QHGPPLTMMETPRQRESLSRSTMTSSGAPQTPHRTFGGKAHVLLAVGGQFLCW 300
Db 241 QHGPPLTMMETPRQRESLSRSTMTSSGAPQTPHRTFGGKAHVLLAVGGQFLCW 300
Oy 301 LPYFSFHLVVALSAOPISITGQVESVVTWIGFCFTSNPFYGCGLNRQIRGELSKQFVCF 360
Db 301 LPYFSFHLVVALSAOPISITGQVESVVTWIGFCFTSNPFYGCGLNRQIRGELSKQFVCF 360

Qy	361	KPAPEELRLSPRESTIENLOFLOGGCSSEWSRPLSPKQEPNADFRPGIAE	420
Db	361	KPAPEELRLSPRESTIENLOFLOGGCSSEWSRPLSPKQEPNADFRPGIAE	420
Qy	421	ETSEFLFOQLSDIIMSDSYRPAASRPLS	451
Db	421	ETSEFLFOQLSDIIMSDSYRPAASRPLS	451

Search completed: December 10, 2002, 09:57:21
Job time : 43 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 09:55:55 : Search time 35 seconds

(without alignments)
2655.064 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318
Sequence: 1 MESSPIPOSSGNSSTLGRVP.....SDIIMSDSYLRAPASPRLES 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp Unclassified: *
15: sp_rvivirus: *
16: sp_bacteriophage: *
17: sp_archaeophages: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2318	100.0	451	4	Q8TDV4
2	435.5	18.8	368	4	Q8TAM0
3	347	15.0	358	11	Q9GX37
4	347	15.0	397	11	Q9D282
5	333.5	14.4	571	6	Q9TWM9
6	330.5	14.3	405	6	Q9GJ56
7	329	14.2	407	6	Q9M200
8	328	14.2	438	11	Q63004
9	327.5	14.1	405	6	Q9GJ70
10	327.5	14.1	405	6	Q9GJ56
11	326.5	14.1	405	6	Q9GJ57
12	322	13.9	399	5	Q9NG02
13	318.5	13.7	402	11	Q9GX46
14	316.5	13.7	559	13	Q9QW71
15	306	13.2	466	4	Q9GRE8
16	304	13.1	515	11	Q9DBL0

17	302.5	13.1	464	5	Q9GQ54	09gg54 aedes aegypti
18	301	13.0	518	6	Q9WY18	09wy18 oryctolagus
19	300	12.9	429	4	Q13729	013729 homo sapien
20	300	12.9	455	4	Q60451	060451 homo sapien
21	300	12.9	499	4	Q13675	013675 homo sapien
22	299.5	12.9	378	4	Q96KH9	096kh9 homo sapien
23	299	12.9	429	6	Q9MZU3	09mzu3 oryctolagus
24	297	12.8	466	4	Q9UD63	09ud63 homo sapien
25	296	12.8	425	6	Q9MZU2	09mzu2 oryctolagus
26	292.5	12.6	603	5	Q9VG57	09vg57 drosophila
27	291.5	12.6	387	4	Q96K10	096k10 homo sapien
28	290.5	12.5	447	6	Q8SPH2	08sph2 sus scrofa
29	289	12.5	446	6	Q8WMD7	08wmd7 bos taurus
30	288.5	12.4	419	5	Q77254	077254 boophilus m
31	287	12.4	466	6	Q9TSM7	09tsm7 sus scrofa
32	284.5	12.3	385	5	Q24038	024038 drosophila
33	283	12.2	407	4	Q75963	075963 homo sapien
34	282	12.2	445	13	Q98841	098841 anguilla an
35	281.5	12.1	407	5	Q9VG54	09vg54 drosophila
36	280.5	12.1	437	13	Q42315	042315 cyprinus ca
37	279.5	12.1	446	13	Q42315	042315 cyprinus ca
38	279	12.0	402	5	Q41198	041198 pongo pygma
39	278.5	12.0	422	6	Q9N296	09n296 pongo pygma
40	278.5	12.0	508	5	Q9VC23	09vc23 drosophila
41	277.5	12.0	349	4	Q9UD67	09ud67 homo sapien
42	277.5	12.0	422	6	Q9N297	09n297 gorilla gor
43	277.5	12.0	474	11	Q8R456	08r456 rattus norv
44	276.5	11.9	422	6	Q9N298	09n298 pan troglod
45	276.5	11.9	445	13	Q98842	098842 anguilla an

ALIGNMENTS

RESULT 1
ID Q8TDV4 PRELIMINARY; PRT; 451 AA.
AC Q8TDV4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative G-protein coupled receptor.
GN GPCR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SOURCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaasu H., Mitaku S.:
RT "Identification of G protein-coupled receptor genes from the human
RL genome sequence."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB083585; BAB89298.1; -
KW Receptor.
SQ
SEQUENCE 451 AA; 49292 MW; 1F477F112E1CEA1A CRC64;

Query Match 100.0%; Score 2318; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 3.8e-194;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MESSPIPOSSGNSSTLGRVQTPEPSTASGVPEVGLDVAASEVALFFMLLDTTAVAGN	60
DB	1	MESSPIPOSSGNSSTLGRVPQTPGSPASGVPEVGLDVAASEVALFFMLLDTTAVAGN	60
QY	61	AAWAAVATKTPALRKFEVPHLCVLDLALTLTLPMLSSALFDHALGGEVACRYLTF	120
DB	61	AAWAAVATKTPALRKFEVPHLCVLDLALTLTLPMLSSALFDHALGGEVACRYLTF	120
QY	121	LSVCFVSLATLSVSAINVERYYVHPMRYEVRRTGLVASVYLGWVKKALAMASVPLG	180
DB	121	LSVCFVSLATLSVSAINVERYYVHPMRYEVRRTGLVASVYLGWVKKALAMASVPLG	180

```

OY 181 RVSMEGAPSVPPGCSLQMSHSAVYCOLFVVVFAVLXFLDLLLVYVCSMFRRVAVAM 240
DB 181 RVSMEGAPSVPPGCSLQMSHSAVYCOLFVVVFAVLXFLDLLLVYVCSMFRRVAVAM 240
OY 241 QHGPPLTWTMTTPQORSLSLSRSTMTSSGAPQTTPHRTGGGKAAYLLAVGGQFLCW 300
DB 241 QHGPPLTWTMTTPQORSLSLSRSTMTSSGAPQTTPHRTGGGKAAYLLAVGGQFLCW 300
OY 301 LPVFSFLVYVALSAOPTSTGVESVYTWIGYFCFTSNPFYGCINROIRGELSOKOYCF 360
DB 301 LPVFSFLVYVALSAOPTSTGVESVYTWIGYFCFTSNPFYGCINROIRGELSOKOYCF 360
OY 361 KPAPEBELRLPSREGSIEENFLQFLOCTGCPSESWSRPLPSKOEPPAVDFRIPQIAE 420
DB 361 KPAPEBELRLPSREGSIEENFLQFLOCTGCPSESWSRPLPSKOEPPAVDFRIPQIAE 420
OY 421 ETSEFLEOQLTSDIIMSDSLPRPASPRLES 451
DB 421 ETSEFLEOQLTSDIIMSDSLPRPASPRLES 451

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RESULT 2

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OBTAMO 08TAM0 PRELIMINARY: PRT: 368 AA.
AC 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
OS G-protein-coupled receptor 62.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN 11
RP TISSUE-BRAIN;
RA Strausberg R.;
DR EMBL: BC026357; AAH26357.1;
KW Receptor.
SQ SEQUENCE 368 AA: 37618 MW: 90506A9D98D12FBA CRC64:

```

Query Match 18.8%; Score 435.5; DB 4; Length 368;
 Best Local Similarity 31.8%; Pred. No. 6.9e-30;
 Matches 127; Conservative 56; Mismatches 144; Indels 73; Gaps 14;

```

OY 40 ASE-----SVALFELLDLTAVAGNAAMVIAITPALRKVFVPHLCVLDLALTIMPL 96
DB 9 ASEVAGSLGLITLAAVEVGALLGNGALLVVRPRGLRDALYLAHLCTVDLAAASIMPL 68
OY 97 AMLSSAL-EDHALFGEVACRLYFLSCFVSALISVSAINVERYYVYVHPMKREYVMT 155
DB 69 GLLAAPPPGGRVRLGPARPCARARFLSAALIPACTIGVALGLARVLYLHPRLPSGRPP 128
OY 156 LGLVASLVGVWVKALAMASVPVLAGRVSWEAGAPSVPPGCSLQMSHAYCOL-----F 208
DB 129 PVL-----VLTAVMAAAGLGLSL-----GPPAPPPA-----PARCSVLAGGLPE 172
OY 209 VVFAVLYELLPLLLILLVYCSMFRRVAVAMOHGPLEPTMETPRORSESLSRSTM 268
DB 173 RPLMALLAFRLPALLLGAGGIFVARRAALR-PPRPA--RGRSLRSLDLSRLSL- 227
OY 269 SGAPQTTPHRT-FGGGKAAYVLLAVGGQFLCWLPYFSFHLVYALSAPSTGVESV 327
DB 228 -----PPLRSRLRPGGKAALAPALAVGQFAACHLPY-----GCACLAAPARAAMEAAYT 276
OY 328 WIGYFCFTSNPFYGCINROIR---GELSOKOYCFKPAPEBELRLPSREGSIEENFLQ 384
DB 277 WVAVSFAFAHPFLYGLQRPVRLALGRLSRRL-----PGVVR----- 314
OY 385 LOGTGCPSESWSRPLPSKOEPPAVDFRIPQIAETSE 424
DB 315 ---ACTPQAMHPRALLQCLQRPPEGPVAVGSPSEAPQTP 350

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RESULT 3

```

OY 42 ESVALFELLDLT-----AVAGNAAMVIAITPALRKVF--FVPHLCVLDLALTIM 94
DB 13 DSIALKVTISVLTTLTIFIVAGVNVVCLAVSLNRRLSTNCFIVSIATDILGLVM 72
OY 95 PLMLSSALFEDHAL---FGEVACRLYFLSCFVSALISVSAINVERYYVYVHPMKRE 151
DB 73 P-----SAITYQSFKWSFGVFCNITSLDVMCLTASILNPLMISDRYCAVTPPLRP 127
OY 152 VRMTGLVASLVGVWVKALAMASVPVLAGRVSWE-----GAPSVPPGCSLQMSHAYC 205
DB 128 VLTTPVRAVLSIVFIWISTISLST--HLGNNSRGTGNDTER--CKQVYV----- 178
OY 206 QLFVVVFAVLYELLPLLLILLVYCSMFRRVAVAMOHGPLEPTMETPRORSESLSRSTM 265
DB 179 EYVGIVDGMVTFYLPRLIMCVYVYRIFKIAREQAKRINHISWMAA----- 224
OY 266 VTSSGAQTTPHRTFGGKAAYVLLAVGGQFLCWLPYFSFHLVYALSAPSTGVESV 325
DB 225 -----TIREHKAFTVTLAAWGAFTVCMPTFAFYRGLRGDAVNEVEGI 271
OY 326 VTWIGYFCFTSNPFYGCINROIRGELSOKOYCFKX-APPEBELRL-----PSREG 375
DB 272 VLMGVANSALNPLIVATLNRDFRMAVYQQLFHCKLASHNHKTSLRLNNSLSRSQREG 331
OY 376 STDENFLQFLOCTGCPSESWSRPLPSKOEPP 407
DB 332 RWOEKPLKLO-----VMSGTELTHPOGSP 356

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Query Match 15.0%; Score 347; DB 11; Length 358;
 Best Local Similarity 27.6%; Pred. No. 3.6e-22;
 Matches 108; Conservative 58; Mismatches 152; Indels 74; Gaps 12;

```

OY 42 ESVALFELLDLT-----AVAGNAAMVIAITPALRKVF--FVPHLCVLDLALTIM 94
DB 13 DSIALKVTISVLTTLTIFIVAGVNVVCLAVSLNRRLSTNCFIVSIATDILGLVM 72
OY 95 PLMLSSALFEDHAL---FGEVACRLYFLSCFVSALISVSAINVERYYVYVHPMKRE 151
DB 73 P-----SAITYQSFKWSFGVFCNITSLDVMCLTASILNPLMISDRYCAVTPPLRP 127
OY 152 VRMTGLVASLVGVWVKALAMASVPVLAGRVSWE-----GAPSVPPGCSLQMSHAYC 205
DB 128 VLTTPVRAVLSIVFIWISTISLST--HLGNNSRGTGNDTER--CKQVYV----- 178
OY 206 QLFVVVFAVLYELLPLLLILLVYCSMFRRVAVAMOHGPLEPTMETPRORSESLSRSTM 265
DB 179 EYVGIVDGMVTFYLPRLIMCVYVYRIFKIAREQAKRINHISWMAA----- 224
OY 266 VTSSGAQTTPHRTFGGKAAYVLLAVGGQFLCWLPYFSFHLVYALSAPSTGVESV 325
DB 225 -----TIREHKAFTVTLAAWGAFTVCMPTFAFYRGLRGDAVNEVEGI 271
OY 326 VTWIGYFCFTSNPFYGCINROIRGELSOKOYCFKX-APPEBELRL-----PSREG 375
DB 272 VLMGVANSALNPLIVATLNRDFRMAVYQQLFHCKLASHNHKTSLRLNNSLSRSQREG 331
OY 376 STDENFLQFLOCTGCPSESWSRPLPSKOEPP 407
DB 332 RWOEKPLKLO-----VMSGTELTHPOGSP 356

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RESULT 4

```

OY 42 ESVALFELLDLT-----AVAGNAAMVIAITPALRKVF--FVPHLCVLDLALTIM 94
DB 13 DSIALKVTISVLTTLTIFIVAGVNVVCLAVSLNRRLSTNCFIVSIATDILGLVM 72
OY 95 PLMLSSALFEDHAL---FGEVACRLYFLSCFVSALISVSAINVERYYVYVHPMKRE 151
DB 73 P-----SAITYQSFKWSFGVFCNITSLDVMCLTASILNPLMISDRYCAVTPPLRP 127
OY 152 VRMTGLVASLVGVWVKALAMASVPVLAGRVSWE-----GAPSVPPGCSLQMSHAYC 205
DB 128 VLTTPVRAVLSIVFIWISTISLST--HLGNNSRGTGNDTER--CKQVYV----- 178
OY 206 QLFVVVFAVLYELLPLLLILLVYCSMFRRVAVAMOHGPLEPTMETPRORSESLSRSTM 265
DB 179 EYVGIVDGMVTFYLPRLIMCVYVYRIFKIAREQAKRINHISWMAA----- 224
OY 266 VTSSGAQTTPHRTFGGKAAYVLLAVGGQFLCWLPYFSFHLVYALSAPSTGVESV 325
DB 225 -----TIREHKAFTVTLAAWGAFTVCMPTFAFYRGLRGDAVNEVEGI 271
OY 326 VTWIGYFCFTSNPFYGCINROIRGELSOKOYCFKX-APPEBELRL-----PSREG 375
DB 272 VLMGVANSALNPLIVATLNRDFRMAVYQQLFHCKLASHNHKTSLRLNNSLSRSQREG 331
OY 376 STDENFLQFLOCTGCPSESWSRPLPSKOEPP 407
DB 332 RWOEKPLKLO-----VMSGTELTHPOGSP 356

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ID          09GJ56
AC          09GJ56      PRELIMINARY;      PRT:      405 AA.
DT          01-MAR-2001 (TREMBLrel. 16, Created)
DT          01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT          01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE          Beta 3 adrenergic receptor.
GN          B3AR.
OS          Ovis aries (Sheep).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC          Bovidae; Caprinae; Ovis.
OX          NCBI_TaxID=9940;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Forrest R.H., Hickford J.G.H.;
RL          "Polymorphism within the ovine beta 3 adrenergic receptor gene.";
RL          Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC          -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC          -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR          EMBL: AF314204; AAC31167.1; -
DR          EMBL: AF314202; AAC31165.1; -
DR          InterPro: IPR000276; GPCR_Rhodopsn.
DR          InterPro: IPR001230; Prenyl_site.
DR          Pfam: PF00001; 7tm_1; 1.
DR          PRINTS: PR00237; GPCRHHODOSN.
DR          PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR          PROSITE: PS00262; G_PROTEIN_REC_P1.2; 1.
DR          PROSITE: PS00294; PRENYLATTON; UNKNOWN_1.
KW          G-protein coupled receptor; Glycophorin; Receptor; Transmembrane.
SQ          SEQUENCE 405 AA; 42928 MW; A0DD3ABEAFB14E75 CR664;

```

Query Match	Similarity	14.3%	Score 330.5	DB 6	Length 405
Best Local	Similarity 29.4%		Pred. No. 11e-20		
Matches 116	Conservative	62	Mismatches 170	IndeIs 47	Gaps 17
QY	7	POSSNSSRTLGHVPQTP--GPST--ASGVEYGLRDVASESYALFEMLDLDTAVAGNNA	62		
DB	3	PMPGNS-S-LTPWDPIDPLPNTANASGLPGPW----AVALAGALLAVALATVGGNLL	57		
QY	63	WNAVLAKTPTALRK--VFVHLCLVDLLAALTLMPLAMISSALDHALFGEVACRLYLE	120		
DB	58	VYVALAKTPRLDTMTNVEFTSLATADLVGLLVVPEG--ATALTGHMPLGVTGCELMTS	115		
QY	121	LSVCEVSLAILSVSAINVRYVVVPHMYEVMTGLVASLVGLVWYVALMASVPVYG	180		
DB	116	VDVLCVTSIETLCAANDRTLAIVNPLRTGALVTKRRARAIVLVWVVAASVAPRAPS	175		
QY	181	RVSMEEGAPSPVPGCSLQWSHSAYCOL----FVVVFAVLYELPRLLLILVYCSMFVA	235		
DB	176	K-WMRYGADAEAGORCH---SNPRCTFASNMVYALLSSVSRYLPDLVWLFYVARYFVA	231		
QY	236	---RYAAMQHCPRLPMWETPR-QNSESLSSSTWYSSGAP-----OTTPHRTFGGG	283		
DB	233	TQRLRLRLRELRERFPPEESPPAPSSGSGPGAPYASPGAVSPYGRAPRLRLPBEH---	288		
QY	284	KAAVVLAAAGGFLCLMLPYFSFHLVVALASQIPISGQVESVYTMIGYCCFSSNPFYGC	343		
DB	289	RALRLTGLIMGFTLCLMLEFFVYVNVNLAGGSLVSGPFTLALNMLGTANSAPNPLY-C	347		
QY	344	LNROIKGLSKQVCFKPAPEEL-----RLPS	372		
DB	348	RSPDFRSAPF-RLILC--RCPRPEEHLAASPPRAPS	379		
RESULT 7					
Q9M200					
AC	PRELIMINARY:		PRT:	407	AA.
Q9M200:					
DT	01-OCT-2000 (Tremblrel. 15, Created)				
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)				
DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)				
DE	Beta-3-adrenergic receptor.				

OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.R., Bidwell C.A., Mills S.E.;
RT "Sus scrofa beta-3-adrenergic receptor (BAR3) gene."
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF274007; AAF62301.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PFO0001; 7tm_1; 1.
DR PRINTS: PR00237; G_PROTEIN_RECIP_FL1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL2; 1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 407 AA; 43610 MW; C659838Z9A8BD09 CNC64;

```

Query Match 14.2% Score 329; DB 6; Length 407;
Best Local Similarity 28.6% Pred. No. 1.5e-20;
Matches 125; Conservative 61; Mismatches 177; Indels 74; Gaps 21;

OY SPIPSSGNSSTGLGHVPQTPGPST-----ASGVEYGLRDVASESYALFFMLLD--L 54
Db 1 111 1111 : 1 11 11:11 11 1
2 APWPQ--GNSS-----LPRPDVSTIAPNNANTSGLPV-----PMVAVALGALLAPVL 49
OY 55 TAVAGNAAVMAVIAKTPALKRF--VFVHCLIVDIALLTMLPLAMISSSALFDHALFGE 112
Db 50 ATVGGNLLVIVAIARTPRLQTMNTNFFVSLATADLVGLLVPPG--TTLALTGHPPLGA 107
OY 113 VACRLYELFSLCFYSLATLSYSAINVEYVYVYVHMREREVMTGLGVASVVGWVKRLA 172
Db 108 TCCELMTSVDVLCVATSIETLICALAVDRILVATNLRIGALTCKRRARAVALVWVSAA 167
OY 173 MASVPLVGLRVSMEEGAPVPPGCSLQMSHSAVCOL-----FVVFAVAVLYFLPLLLLV 227
Db 168 VSPAFINSK--MMRGADADAQRCH--SNPSCCTPASMMPALLSSSVFLPLLVMLFV 223
OY 228 YCSMRVAVKVAAMOHGRLPTW--MTPPQRBESLSRSTNWTSSCAPOTTHRTPTGGSKA 285
Db 224 YARVF---VYATSQLRLRLMELSRFPPEESPAPRSRS--QSPADRPMPSPAGVPSHGRR 278
OY 286 AVLLV-----AVGGOLFICMLPYPSFHLVYVLSAQPISTGQVESVYTMIGYEC 333
Db 279 PARLLPLEHNRALCTGLIGIMGFTLICMLFFVYVNVVNRALGGBSLPVPAFLALNMLGTAN 338
OY 334 FTSNPFYGCNLNROIRGELSKQVCFPPAPEEELRL--PSNEGSIIEENFLOFLOGTGCP 391
Db 339 SAFNPLV--CHSPDRSAF--RRLLC--RCGPEEHLLAASPPRAPS-----GAP 382
OY 392 SESVSRPLPSPKQDEPP 408
Db 383 ET--LTHPAES--ROSP 396

RESULT 8
O63004
ID O63004 PREDIMINARY; PRT; 438 AA.
AC O63004;
DT 01-NOV-1996 (TREMBLrel. 01, created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE 5-HT6 serotonin receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=STRATUM;
RX MEDLINE=96102917; Pubmed=8522988;

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RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
 RA Meltzer H.Y., Shibley D.R., Roth B.L., Hamblin M.W.,
 RT "Cloning, characterization, and chromosomal localization of a human 5-
 RT h76 serotonin receptor."
 RL J. Neurochem. 66:47-56(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: L41146; AAA92633.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PRO0237; GPCRHHODOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 DR PROSITE: PS00294; PRENYLATION; UNKNOWN.1.
 KM G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 438 AA; 46786 MW; DB9040389269149 CRC64;

Query Match 14.2%; Score 328; DB 11; Length 438;
 Best Local Similarity 27.4%; Pred. No. 2e-20;
 Matches 129; Conservative 61; Mismatches 184; Indels 96; Gaps 19;

QY 2 ESSPIPOSSGSSITGLRVPQTPGSPSTASGVPEGLRDVASESVALFEMLLDLTAVAGNA 61
 DB 4 EPGV-----NSST---PANGPPPPAPG-----GSGWVAALCVYVLTVA-AANS 45
 QY 62 AVMAVIARTPALRKF--VFVPHLCVLDLALTLPLAMLSAALPDHALGEVACRLYL 119
 DB 46 LLIVLTGTPAVRNTSNFELVSLFTSDLMGLVMPAPML--NALIGRWVLARGLCLLMT 103
 QY 120 FLVCFVSLAISVAINVERIYVHPMYREVRMTGLVASVLGVWVKALMAASVPL 179
 DB 104 AFDMCCSASILNCLISLDRIYLLITSLPKRYKLRMTAPRALALITGLAMSLAALASPL 163
 QY 180 GRWSME--GAPSPV--PCGSIOWSHSAVCOL-----FVVPVAVLYELLPLLLIIVYCSMF 232
 DB 164 --LGMHLGLGARPPAPG-----OCRLASLPFVLVASGVTFPLPSGALICTYCRIL 212
 QY 233 RVARVAAMOGPLPTVM-----ETPRGSESLSSSTWVSSGAPQTPPHRTFG 281
 DB 213 LAARKAVQVAVSLTTGAGALETLQVPRTPRPMESADSRLATKISRAKL-----264
 QY 282 GGAAVVLLAVGQFLCMLPYEFSEHLYVALSAQPISTGOVESVVMVIGYFCFTSNPEFY 341
 DB 265 --KASLTGLIGMFEFTWLPFEVANIAQAV--CDCISPLGFD-VLTWLGVCNSTMNPDIY 320
 QY 342 GCUNROIRGELSKQFVCFKPAPBE-----LRLP-----371
 DB 321 PLFMDFKRALGRPLPCVHCP--PEHRASPAKSPKMTSHSGARGLSLQVLPPLPNSD 379
 QY 372 SREGSIEENFLQFLOGTGPSESVWSRPLSPKQEPVAVDFRIPGQIAEE 421
 DB 380 SDSASGTSGLQLTQALLPGEA--TRDPPPTPATIVVNFVYDSVEPE 427

RESULT 9
 O9GLJ0 PRELIMINARY; PRT; 405 AA.
 AC O9GLJ0;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Beta 3 adrenergic receptor.
 GN B3AR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Forrest R.H., Hickford J.G.H.;
 RT "Ovis aries beta 3 adrenergic receptor (B3AR) gene - allele F,
 RL complete cds."
 CC Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RA Forrest R.H., Hickford J.G.H.;
 RT "Polymorphism within the ovine beta 3 adrenergic receptor gene."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF314205; AAC31168.1; -
 DR EMBL: AF314201; AAC31164.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR001230; Prenyl_site.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PRO0237; GPCRHHODOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 DR PROSITE: PS00294; PRENYLATION; UNKNOWN.1.
 KM G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 405 AA; 42956 MW; 6C9F81EBAF3C578 CRC64;

Query Match 14.1%; Score 327.5; DB 6; Length 405;
 Best Local Similarity 29.4%; Pred. No. 2.1e-20;
 Matches 116; Conservative 61; Mismatches 171; Indels 47; Gaps 17;

QY 7 POSSGSSITGLRVPQTP--GPST--ASGVPEGLRDVASESVALFEMLLDLTAVAGNA 62
 DB 3 PMPGNS--LTPWDFITLAPNTANASGLRVPW-----AVALGALLAVLATVAGNL 57
 QY 63 VMAVIARTPALRKF--VFVPHLCVLDLALTLPLAMLSAALPDHALGEVACRLYL 120
 DB 58 VIVARTPLQGTNTVNTFVSLATADLVGLVPPG--ATLALTGHPHLCVTCCELMTS 115
 QY 121 LSCVFSALISVAINVERIYVHPMYREVRMTGLVASVLGVWVKALMAASVPLG 180
 DB 116 VDVLCVTAASLETCLALVDRLATVNPRLRGALVTKRRAAAVVLWVSAVSFAPIMS 175
 QY 181 RVSWEGAPSPVPCGSIOWSHSAVCOL-----FVVPVAVLYELLPLLLIIVYCSMPRVA 235
 DB 176 K-WRVGADAENQCH---SNPRCTFASNMPYALLSSVSFYPLVLMFLVAVRYVA 231
 QY 236 ---RVAMOHGPLPTMETPR--ORSESLSSRSMTVSSGAP-----QTPPHRTFGG 283
 DB 232 TROLRLRLRELGRPPPEPSAPPSRSGSPGACPVASPVGYGRPARLLPREH---288
 QY 284 KAAVVLAVGQFLCMLPYEFSEHLYVALSAQPISTGOVESVVMVIGYFCFTSNPEFYGC 343
 DB 289 RALRTGLIGMFTPLCMLPFEVAVVVRALGGPSLVSGTFIALMWGLANSAPNPLIY-C 347
 QY 344 LNRQIRGELSKQFVCFKPAPBEEL-----RLPS 372
 DB 348 RSPDFRSAP--RLLC--RCPEEHLAASPPRAPS 379

RESULT 10
 O9GLS6 PRELIMINARY; PRT; 405 AA.
 AC O9GLS6;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Beta 3 adrenergic receptor.
 GN B3AR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Forrest R.H., Hickford J.G.H.;
 RT "Polymorphism within the ovine beta 3 adrenergic receptor gene."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.


```

0Y      23  PGPSTASCPVPGVGRADVASSVLLFELLDDLTAVAGNAAVAALAKPALB-KEVEVE 80
      23  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      23  PEETGSLP---VWEAAASLTLGLV---LATVCGMLVILSVFTTRPLRIYONFIV 76
      23  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

0Y      81  HLCVLDLALTLMLPLMLSSSLAFDHALFEGEYACRLYLFSCEVSLALISVAIINER 140
      81  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      77  SLAVADLAVAILVMPFV-AYLLGKWFEGHLCRKLTCVOLCCTASLMLCALDR 134
      77  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

0Y      141  YYYVHHMRKEVRKTLGLVASVLVGVWYKALAMASVPVLGRVW-BEGAPSVPECCSLQW 199
      141  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135  YMATDEINYAOKRTLKRVLATTAGVWILSGAISSPPLGAMDWELEPEGP----- 187
      135  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

0Y      200  SHSAYCOL-----FYVYFAVLXFLPLLLILVYYGCMF-----RVARVAMQ-- 241
      200  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      188  ----COLTRQGVIVYSSIGSFPIPLMLSLVLEIYLATRRRLRERAROSIRIAVOST 242
      188  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

0Y      242  -----HGPLPTWMEETPROSES--LSRSMTVSSGAPOTPHRTFEGG 282
      242  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      243  RHREADDAAESVSSETHNNE---RSIPRPHAKPSLIDPELVEITGGGTTSSKRITGS 298
      243  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

0Y      283  -----GKAAYVLLAVGQFLLCMLPYFSFHLVYALSAOPIS 318
      283  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      299  RAAATTTTVYOFIEBORIRISLKERRAARLFIYIMGVFVCMLEPFLMYIVPFCDCCP 358
      299  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

0Y      319  TGOVESVVTWIGYCFSTSNFFGCLNQR 349
      319  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      359  SDRMVYFITWLGIVNSALNPLIYITINDYR 389
      359  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Query Match	13.7%	Score 318.5	DB 13	Length 402
Best Local Similarity	27.7%	Pred. No. 1.2e-19		
Matches 96	Conservative 69	Mismatches 145	Indels 37	Gaps
26 STAGVPEVGLRDVASEVALPFMLLDLDLAVAGNAAVMVAIAKTPAL--RKFEVVFHLC 83				
Db 12 NSTGGLDNGL--WLEVSIIIIAIL--ACAGNLIVYVTLKKPKYLLTPSNKKEVFSLT 66				
0Y 84 LVLDLALVLTPLAMSSSALLFDHALFGEVACRLYFLFSVCFVSLAISVSAINVERYY 143				
Db 67 SSNLLSLVLMLEFVVAAS--VRDWMGVYWCNFTALLHLVSSSSMILGAIADRYYA 124				
0Y 144 VVHEPMREVRKRTGLGLVASVYGVVKNLAASVPVVG-----RVSMEGAPSVPPGCS 196				
Db 125 VLYEMITPKTKTGRNALVAILYIMHSLVGCLEPPLDGMSSPEFDRKKWT-----CT 175				
0Y 197 LQMSHSAVCLQEVVVEAVLYFLPLLLILLVVYCSMFVRVA--MONGPLPTMMETPRO 254				

[illegible]

RESULT 14			
ID	090W71	PRELIMINARY;	PRT; 559 AA.
AC	090W71;		
DT	01-MAY-2000 (TREMBLrel, 13, Created)		
DT	01-MAY-2000 (TREMBLrel, 13, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel, 20, Last annotation update)		
DE	Alpha 1-adrenergic receptor subtyp alpha 1D, alpha 1D-AR.		
OS	Rattus sp.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
OX	NCBI_TaxID=10118;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9210054; PubMed=1661838;		
RA	Perez D.M., Plascik M.T., Graham R.M.;		
RT	"Solution-phase library screening for the identification of rare		
RL	clones: Isolation of an alpha 1D-adrenergic receptor cDNA.";		
RL	Mol. Pharmacol. 40:876-883(1991).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	InterPro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.		
KW	G-protein coupled receptor; Glycoprotein; Transmembrane.		
SO	SEQUENCE 559 AA; 59739 MW; 37CD9BD696D3A47D CRC64;		

	Query Match Similarity	13.7%	Score 316.5;	DB 11;	Length 559;
	Best Local Similarity	26.1%	Pred. No. 2,7e-19;		
	Matches 102;	Conservative	76;	Mismatches 156;	Indels 57; Gaps 15;
Oy	6	IPOSSGNSSTL---	GRVPQT---	PGPSTA---	SGVPEVLGRDVASGSVAL--FFMLIID 53
		:::::	:::::	:::::	:::::
Dd	42	VPGATGGGVGTGGGEIIOSSSTGEPGAASAAGEVGSAAVGGLVAAGLVSAQGVGVAFI 101			
Oy	54	LTAAVGNMAVMNVIKTPTALRKFV--FEFHLCYLDVLAALTPLMPLAMSSALFPHALEG 111			
			:	:	:
Dd	102	LTVAGNLLIVILSACNRHLOQVTWTFEYNLAVALDILLSAALFPS--ATMEVLGFMAFG 159			
Oy	112	EYACRLTYFLSYCEVSLAISVSAINVERYYYVHPMRIYEMRTGLVASVLGVWVKAL 171			
		: :	:	:	:
Dd	160	RTEFCVMAADVCLCTASTLSICTSVDRYRVGRSLKPAIMIERKAAIIALLMAVAL 219			
Oy	172	AMASVPVLGRVSMEGEASVPPGCISLOWSHSNVCOL-----FVVVFAYLYFLPLLILYL 226			
		:	:	:	:
Dd	220	VVSVEPLLG---WKI---PVPP-----DERFCITEEVGAIINSSVCSFYLLPMNAVIV 266			
Oy	227	UYCSMFRRAR--VAAMOGCPLEPTMETPRORSE-----SISSRSNTWYTSSCAP--QTTPHRT 279			
		: : :	:	:	:
Dd	267	MICRYVYAARSTRTRSLLEG---IKREPKASEVLRIRHCARTASAKYPGTOSCKHT 322			
Oy	280	FEGGG-----KAAYVLLAAGGOFILCWLMEYFSHFHLVALSAOPISTGOESVYT 327			
		:	:	:	:
Dd	323	LKSLSVRLRKRSREKKAKKATLAIYGVJLWMPFFLFYLPGLGISIFPQIKPBEGVFKVIF 382			
Oy	328	WTGYFCFTSNPFYCGLNROINGELSKOFCV 358			
		:	:	:	:
Dd	383	WGIYFNSCVNPLITYPCSSREFKRARFLRLLC 413			

RESULT 15

```
Q96RE8      PRELIMINARY:      PRT:      466 AA.
ID  Q96RE8
AC  Q96RE8:
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Adrenergic receptor alpha-1a.
GN  ADRA1A.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Banerjee A.G.N., Aarlt A.;
RT  "RT-PCR cloning and sequence analysis of adrenergic receptor subtype-
RT  alpha-1a cDNA from human prostate cell-line DU-145.";
RL  Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF395806; AAK77197.1;
DR  InterPro; IPR000276; GPCR_Rhodopsn.
DR  Pfam; PF00001; 7tm.1.1;
DR  PROSITE; PS00237; G-PROTEIN_RECP_F1_1; UNKNOWN_1.
DR  PROSITE; PS50262; G-PROTEIN_RECP_F1_2; 1.
KW  Receptor.
SQ  SEQUENCE      466 AA;  51431 MW;  876CBFB3E323B7A1 CRC64;

Query Match      13.2%;  Score 306;  DB 4;  Length 466;
Best Local Similarity 27.8%;  Pred. No. 1.8e-18;
Matches 110;  Conservative 62;  Mismatches 133;  Indels 90;  Gaps 18;

QY  10  SGNSSTLGRVPQTGPGSTASGVPEVGLRDVASEVALFPMFL--LDLTAVAGNAAMAVI 67
DB  5  SGNASDSSNCTQPPAPVNIS-----KAILGVILGGLIFGVGNILVILSV 51
QY  68  AKTPALRKEV--FVFHLCLVDLALTLTLMPLMLSSALFD--HALFGEVACRLYDLFS 122
DB  52  ACHRHLSVTHYIYNLAVDLTLSTVLPF----SAIFEVLGYMAFGRVFCNIMAAVD 106
QY  123  VCFVSLAILSVSAINVERYYVYVPMRYEVRMT--LGLVASVLGVVVKALAMASVPVLG 180
DB  107  VLCCTASIMGLCIITIDRYIGVSHPLRYPTIVQRRGLMA--LLCVWALSLVISIGPLFG 164
QY  181  RVSMEGAPSPVPGCSLQMSHSAYCOL-----FVVVFAVLYFLPLLLILVVYCMFRA 235
DB  165  ---WRQAP-----EDFTICQINERGVLYFSALGSFYLPALAILVMYC---RVY 208
QY  236  RVAAMOHGPLPTMETPRORSESLSSRSTWVTSSGAP-----QTPH-----RTF 280
DB  209  VVAKRESRGLSKGLTKDSSEQVTLR---IHRKNAPAGSGSMASAKTKTHFSVRLKFS 265
QY  281  GGGKAAAVLLAVGGQFLCMLPYFSFHLVYALSA-----QPISTGOVESVWTWGYFCFT 335
DB  266  REKKAATFLGIWGCFLCMLPFP--LVMPIGSFPDPKPSFT--VFKIVFWLGYLNSC 320
QY  336  SNPFYVGLNRIQGLSKQVFCFFKPAPEELRL 370
DB  321  INPIIYPCSSQE-----FKKAFQNVLR 343
```

Search completed: December 10, 2002, 09:58:24
Job time : 37 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 10, 2002, 09:56:20 : Search time 21 seconds
(without alignments)
2064.601 Million cell updates/sec

Title: US-09-838-028-2

Sequence: 1 MESSPPIPOSSGSSSTRIGRVP.....SDIIMSDSYLRPAASPRLES 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR-73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	823	35.5	428	2	I51087	G protein-coupled
2	351	15.1	358	2	JQ1278	histamine H2 recep
3	349.5	15.1	440	2	JC5520	serotonin receptor
4	349	15.1	359	2	A39008	histamine H2 recep
5	343	14.8	359	2	JC4120	histamine H2 recep
6	340	14.7	359	2	JH0449	histamine H2 recep
7	338.5	14.6	436	2	JN0591	serotonin receptor
8	337	14.5	400	2	A53281	beta-3-adrenergic
9	336	14.5	400	2	A41679	beta-3-adrenergic
10	335.5	14.5	405	2	S65459	beta-3-adrenergic
11	335	14.5	428	2	A55044	beta-4C-adrenergic
12	332.5	14.3	572	2	I39369	alpha-1A-adrenergic
13	329.5	14.2	437	2	I57942	5-hydroxytryptamin
14	326.5	14.1	400	2	S32804	beta-3-adrenergic
15	324	14.0	414	1	ORH0B3	beta-3-adrenergic
16	322.5	13.9	418	2	G02953	beta-3-adrenergic
17	322.5	13.9	560	2	A38731	alpha-1A adrenergic
18	320	13.8	501	2	JH0447	alpha-1A-adrenergic
19	319.5	13.8	408	1	ORH0BE	beta-3-adrenergic
20	317.5	13.7	379	2	JC6178	serotonin receptor
21	308	13.3	517	2	A45121	alpha-1B adrenergic
22	305	13.2	515	2	A40491	alpha-1B adrenergic
23	300	12.9	429	2	S65656	alpha-1C-adrenergic
24	300	12.9	466	2	JN0765	alpha-1C-adrenergic
25	300	12.9	499	2	S65657	alpha-1C-adrenergic
26	292.5	12.6	564	2	A38271	serotonin receptor
27	292	12.6	466	2	I57959	alpha-1C adrenergic
28	291.5	12.6	515	2	JC1525	alpha-1B-adrenergic
29	291	12.6	477	2	S71323	alpha-1A adrenergic

30	290.5	12.5	501	2	T18863	hypothetical prote
31	290	12.5	466	2	A35375	alpha-1-adrenergic
32	289.5	12.5	398	2	JN0505	somatostatin recep
33	285	12.3	446	1	DYH0D1	dopamine receptor
34	284.5	12.3	385	2	S68780	dopamine D1-like r
35	283	12.2	446	2	I47217	dopamine receptor
36	281.5	12.1	384	2	A47249	brain-specific som
37	278	12.0	459	2	A56649	dopamine receptor-
38	277.5	12.0	422	2	I38209	serotonin receptor
39	277.5	12.0	483	2	A25896	beta-adrenergic re
40	277.5	12.0	511	2	S44275	dopamine receptor
41	274	11.8	387	2	I49246	D4 dopamine recept
42	272	11.7	444	2	C55886	dopamine receptor
43	271.5	11.7	448	2	A47519	serotonin receptor
44	270.5	11.7	384	2	JC4529	somatostatin recep
45	270	11.6	402	2	I56595	neurokinin 2 recep

ALIGNMENTS

RESULT 1

I51087

G protein-coupled seven-transmembrane receptor - Japanese medaka

C:Species: Oryzias latipes (Japanese medaka)

C:date: 13-Sep-1996 #sequence: revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51087

R:Yasunaka, A.; Abe, K.; Saigo, K.; Arai, S.; Emori, Y.

Biochim. Biophys. Acta 1235, 467-469, 1995

A:Title: Molecular cloning of a fish gene encoding a novel seven-transmembrane recept

A:Reference number: I51087, MUID:95275927, PMID:7756357

A:Accession: I51087

A:Status: preliminary; translated from GB/EMBL/DBET

A:Molecule type: DNA

A:Residues: 1-428 <YAS>

A:Cross-references: GB:D43633; NID:9992581; PIDN:BAA07741.1; PID:9992582

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 35.5%; Score 823; DB 2; Length 428;
Best local similarity 42.3%; Pred. No. 3.5e-59;
Matches 184; Conservative 81; Mismatches 142; Indels 28; Gaps 11;

QY	2	ESSPI---POSSGSSST--LGRVPQTGPSTASGVPEVLG----	RDVASSEVALFFLL 52
DB	5	KTSPMITSDSISNFTGFGPHPTVP-----PDVGVTSSQSKDLFGFCVTL 56	
QY	53	DLTAVAGNAVMVAIAKTPALRKFEVFEHLCLVDLALTLPLMLSSALFDHALFGE 112	
DB	57	NLIALANTGVMAIAAPHLKFAFYCHLCANDVLCAILMLPLGITSSSPFRTVFTI 116	
QY	113	VACRLYLELVCVSLAITSVAINVERYYVHPMYREYMTGLVAVLVGVAKALA 172	
DB	117	LECGVYIFLNVFLWILITITATISVERFYVHPMYREYMTGLVAVLVGVAKALA 176	
QY	173	MASVPVIGRVSWMGASVPGCSLWMSHAYCOLFFVFAVLYFLPLLLLVVYCSMF 232	
DB	177	LAVLTLEGPWPYGHQSSIAASHCSLASHSRLCRVFAVLCVLCFLAVVIVISVAVY 236	
QY	233	RVARVAMOHGP--LPTMET--PROSESLSSRTWTSGAOP--TPHRTFGGKAAYV 288	
DB	237	KVARSAALQOVPAVPTAADSPAKDRSDINSQTTITTTTTLVQRLSPERAFFSGKALY 296	
QY	289	LAVAGQFLLCWLPYFSEHLYVALSAOPISTGOVESVVTWIGYFCFTSNPFYGCCLNRQI 348	
DB	297	LAFIVGQFLVCWLPYFSEHLYVALSAOPISTGOVESVVTWIGYFCFTSNPFYGCCLNRQI 356	
QY	349	RGELSK-QVCFKRPAPAEELRLPSSRGSTIEENTLQLOGTGCPSESWVSRPLSPK-QE 406	
DB	357	RDELVKKRRCCVQVQV---BIGPSLSGSGFOENLQIORTSSSETHPSFANSNPRNME 413	
QY	407	PPAVDFFPGQIAEE 421	

Db 414 NOA-HKIPQIPPEE 426

RESULT 2

histamine H2 receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: J01278

R:Ruat, M.; Traiffort, E.; Arrang, J.M.; Lours, R.; Schwartz, J.C.

Biochem. Biophys. Res. Commun. 179, 1470-1478, 1991

A:Title: Cloning and tissue expression of a rat histamine H2-receptor gene.

A:Reference number: J01278; M0ID:92028890; PMID:1930188

A:Accession: J01278

A:Molecule type: DNA

A:Cross-references: GB:S57565; NID:q236183; PIDN:AA019935.1; PID:q236184

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:22-45/Domain: transmembrane #status predicted <TM1>

F:58-81/Domain: transmembrane #status predicted <TM2>

F:93-113/Domain: transmembrane #status predicted <TM3>

F:136-159/Domain: transmembrane #status predicted <TM4>

F:178-203/Domain: transmembrane #status predicted <TM5>

F:234-260/Domain: transmembrane #status predicted <TM6>

F:267-288/Domain: transmembrane #status predicted <TM7>

F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:220,311,315/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 15.1%; Score 351; DB 2; Length 358;

Best Local Similarity 27.5%; Pred. No. 6, 2e-21;

Matches 106; Conservative 58; Mismatches 150; Indels 72; Gaps 12;

43 SVAFPLLLDLTAAGNAVMIAKTPALRFV--FVHCLDVLDAALTLPLMLLS 100

22 SVVLTLLIL--TIAGNVVCLAVSNRLRLSTNCFIYSLATDILLVLVP---- 74

101 SSALFDHAL--EGEVAQLYFLVSCFVSLAISVAINVERYYVHBMRYEVRMTLG 157

75 -SAIYQLSFMWSEGFHCNITYSLDVMLCYASILNFMISLDRCAYTDPLRPVLTVP 133

158 LVASVLYGVVAKLMAASVYLVGRVSE-----GAPSPFGCSLQMSANCOLFVV 211

134 RVALISLVFIWVITLSELSI--HLGNSSRNGTRGCGNDTRK--CKQVNV-----EYGLV 184

212 FAVLYELLPLLLLVYCSMFARVAVAMOGPLPTWETPRORSELSRSRTMTSSGA 271

185 DGLVTEYLLPLLCVYTRIFKTAAREGAKRINIISSKAA----- 224

272 POTTPTHTGGGKAAYVLLAVGGQFLCWLPIYFSFHLVYALSAPISTGQVESVWTWIGY 331

225 -----TIREHKATVTLAIVMGAFITICMPYFAPYRGRLRGDAINEAVEGIVLWLG 277

332 FCFSTSNPFEGCLNROIRGELSKQVCFEFP--APEEELN-----PSREGISTENF 381

278 ANSALNPILVLAALNROFRTAYQQLFHCKFASHSHKSTLRLNNSLLPRSQSREGRMQEEK 337

382 LQFLQGTGCPSESWSRPLSPKQEP 407

338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

Db 338 PLKLG-----VMSGTELTHTPOGNP 356

A:Accession: J05520

A:Molecule type: mRNA

A:Residues: 1-440 <KOH>

A:Cross-references: GB:L41147; NID:q1162923; PIDN:AA092622.1; PID:q1162924

A:Experimental source: brain

C:Comment: This protein shows high affinity for several therapeutically important ant

C:Genetics:

A:Gene: HTR6

A:Map position: 1p35-36

A:Intons: 238/3; 291/3

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran

F:28-51/Domain: transmembrane #status predicted <TM1>

F:65-88/Domain: transmembrane #status predicted <TM2>

F:100-123/Domain: transmembrane #status predicted <TM3>

F:143-166/Domain: transmembrane #status predicted <TM4>

F:185-208/Domain: transmembrane #status predicted <TM5>

F:266-289/Domain: transmembrane #status predicted <TM6>

F:298-321/Domain: transmembrane #status predicted <TM7>

F:10/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 349.5; DB 2; Length 440;

Best Local Similarity 30.7%; Pred. No. 1e-20;

Matches 127; Conservative 59; Mismatches 171; Indels 57; Gaps 18;

19 VPOTPGSTASGVPEVGLRDVASES---VALFFMLLDLTAVAGNAVMIAKTPALR 74

2 VPE-PCR-TANSTPANCAGPSAPGSGWAAALCVIALTA-AANSILALICTQPALR 58

75 KF--VFVHCLDVLDAALTLPLMLSSALFDHALFGEVACRLYFLTSCFVSLAIS 132

59 NTSNFFLVSTSDLLWGLVMPAML--NALYGRWLALGCLLTWAFVDMCCSAILN 116

133 VSAINVERYYVHBMRYEVRMTLGVLASVLYGVVAKLMAASVYLVGRVSE-----GAP 189

117 LCILSDRYLLILSLPKYKLMPTLRALALVLAWSIALASTLPPL--LGMHELGHAR 174

190 SVPPGSLQMSHSAVYCOLFFVFAVLYFLPLLLLVYCSMFARVAVAMOGPLPTWM 249

175 PVRGQCRLLASLP-----FVLVASGLTFLFPGALICETCYRIILAAKQAVQVASTTGM 229

250 -----ETPRORSELSRSRTMTSSGAPOTTPTHTGGGKAAYVLLAVGGQFL 298

230 ASQASETLQVPRTRPGVEADSRRLATKHSRAL-----KASLTGLTILMFFV 279

299 CMLPYSEFHLVYALSAPISTGQVESVWTWIGYFCFTSNPFEGCLNROIRGELSKQVFC 358

280 TWLPFVYANIVQAV--CDCISPGFLD-VLTWLGICNSTMPITPLMKRDKRALGR----- 333

359 FFKPABEELRLP--SREGSIEENFLQGTGCPSESWSRPLSPKQEP 411

334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

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Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

Db 334 -FLPCP-----RCPRERQASLASPSLRSHSGPRGLS-LQGVLPPLP--PPDS 379

[illegible]

RESULT 7
 JN0591
 serotonin receptor 6 - rat
 N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT₆)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
 C:Accession: JN0591
 R:Author: M.; Traiffort, E.; Arrang, J.M.; Tardivel-Lacombe, J.; Diaz, J.; Leurs, R.; Schw
 Blochem. Biophys. Res. Commun. 193 268-276, 1993
 A:Title: A novel rat serotonin (5-HT₆) receptor: molecular cloning, localization and str
 A:Reference number: JN0591; MUID:93277562; PMID:8389146
 A:Accession: JN0591
 A:Molecule type: DNA
 A:Residues: 1-436 <RUA>
 A:Cross-references: GB:562043; NID:g385708; PIDN:AA026908.1; PID:g385709
 C:Genetics: 238/3
 A:introns: 238/3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
 F:29-53/Domain: transmembrane #status predicted <TM1>
 F:63-84/Domain: transmembrane #status predicted <TM2>
 F:95-122/Domain: transmembrane #status predicted <TM3>
 F:141-168/Domain: transmembrane #status predicted <TM4>
 F:185-213/Domain: transmembrane #status predicted <TM5>
 F:267-293/Domain: transmembrane #status predicted <TM6>
 F:297-319/Domain: transmembrane #status predicted <TM7>
 F:9/Binding site: carbonylate (Asn) (covalent) #status predicted
 Query Match 14.6%; Score 338.5; DB 2; Length 436;
 Best Local Similarity 28.4%; Pred. No. 8e-20;
 Matches 129; Conservative 58; Mismatches 171; Indels 97; Gaps 20;

Query Match	14.66:	Score 338.5:	DB 2:	Length 436:
Best Local Similarity	28.44:	Pred. No. 8e-20:		
Matches 129:	Conservative 58:	Mismatches 171:	Indels 97:	Gaps
Qy	2	ESSPPOSSGSSPTLGRVPOPGPSTASGVEVGLRDVASEVALFFMLLDLTAVAGNA	61	
	:			
Db	4	EPGPV-----NST--PAMCGPPAPG-----GSGWVAALCVYIVLTA-AANS	45	
Qy	62	AVMAVIATPPALRRF--VFVPHCLVDLALTLPLMLSSSALFDHALFGEVACRLYL	119	
	:::	:		
Db	46	LIIYLICQPLRLRMTSNFVLVSLFTSDLMGVLVMPAML--NALYGRVILARCLLMT	103	
Qy	120	FLSYCFVSALISVSAINVERRYVVVPHMRVEVMTGLVASVLGVWVALAMASVPL	179	
	:	:		
Db	104	AFDWMCGSASTLNLCISLDRIYLLISPLRKLRLMTAPRALALILGMSLALASLPRL	165	
Qy	180	GRVSMEE-GABSV-PGCSLOMSHAYCOL----FVVVFAYVLELLPRLLEILVYCSMF	232	
	:	:		
Db	164	--LGMHELGRKRRPARG-----QCRLLASLPFLVAVASGVFFFLPSGLICTTYRIL	212	
Qy	233	RVARVAAHQGRPLETWM-----ETPRROSESLSRSTVNTSSGAPQPTPHRTFG	281	
	:			
Db	213	LAARKQAVQVASLTITGAAGALLETLOYRPRPRGEMESADSRLATKHSKRAL	264	
Qy	282	GKKAAYVLLAVGQFLLCWLPRYFSFHLVVALSAOPISTGOVESVVTWIGYFCFTSNPFY	341	
	:	:		
Db	265	--KASLTGLIGLGMFEFTWLPFLFVANIAAOAV-CCDISPGLFD-VLTWIGYCNSTMPNDIY	320	
Qy	342	GCLNRQIRGELSKQFVCFKAPAEDELRLP-----SREGSI	377	

Db 321 PLFMRDEFKRLAGRLPCVHCP-PEHRPALPPPGCGPLTANVPDASACRCLCLCKROTQI 379

Qy 378 EENFLQFLQGT--GC---PSESWSRPLPSKQEP 407

Db 380 QTP----LQGAAPRACSSQPSFCCLERPEPTGRNPP 410

RESULT &

beta 3-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)

C:/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:/Accession: A53281; S29808

R;Granneman, J.G.; Lahners, K.N.; Chaudhry, A.
Mol. Pharmacol. 40, 895-899, 1991

A:Title: Molecular cloning and expression of the rat beta 3-adrenergic receptor
A:Reference number: A53281; MUID:92100057; PMID:1664635

A;Accession: A53281
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-400 <GRA>

A/Cross-references: GB:S73473; NID:g241215; PIDN:AAB20702.1; PID:g24121616
A/Note: sequence extracted from NCBI backbone (NCBIN:73473, NCBI:P:73476)

R: Bensaid, M.; Kagnad, M.; Rodriguez, M.; Le Fur, G.; Caput, D.
FEBS Lett. 318, 223-226, 1993

A; title: The rat beta3-adrenergic receptor gene contains
A; Reference number: S29808; MUID: 93178631; PMID: 8382630

A;Accession: S29808
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-400 <BE

A: Cross-References: GR: S5648; NID: G298306; PID: AAB25520.1; PID: G298307
C: Superfamily: vertebrate rhodopsin

Keywords: G protein-coupled receptor; transmembrane protein; superfamily; vertebrate inopsin

Query Match	14.58;	Score 337;	DB 2;	Length 400
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Best Local Similarity 28.2%; Pred. No. 9,6e-20;
Matches 120; Conservative 65; Mismatches 188; Indels 52; Gaps 17,

Q7 4 SPIRSSGNSSTLGRVPQ-TPGPSTASGYPEVGLRDVAESEVALFMYLLDLDLTAVAGNAA 62

Dd : - - - - - | - - - - - | - - - - - | - - - - - |
2 APRHHKGSGLAFSDAPRTLPDSAMTSGIPGV-----PPAALLAALLALTGGNL 54

QY 63 VMAYIAKTPALRKF--VFVFLCLVDLLAATLMPPLAMSSALEFDNALPGEVACRLYL 120
| : ||||| : ||| | : ||| :: || | - | :
Db 55 VITLARPRPLOTTFNNFVSLADLVGLNPPG--ATLATGMPIRGATCGCEIMTS 112

QY 121 LSYCFVSLAITSVAINVERYYYVHPHRYEVRMTIGIVASVLGVWVKALAMASVPVLG 180

```
Db      113 VDVLGVTSIETICALAVDRYLAVTNPLRYGTLVTKRRARAAYLVLIWIVSATVSEFAPIMS 177
```

QY 181 RVSNIEGAPSVPPGCSLQWMSHAYCQL-----FVVFAYLYELLPLLLLVVYCSMFRVA 23

```

Db      173 Q-WMRVGDADAEAQECH--SNPRCSFASNMPYALLSSVSFYLLPLVLMIFYARVFVVA 22
      :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

2Y 236 ---RVAAMQHGPLPTMETPR--QRSESLSSRSTMTSSGARQ--TTPHR--TFGGCKA 28

```

Db      229 KRGRLLRRELGRPP-EESPRSPSRSPAPVGTPTASDGVPSGRRPARLLPLGENHRA 28
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

286 AVLLAVGGQFLLCMPYFSFHLVVALSAQPISTGVESVTWIGYFCFTSNPFYGLN 34

Db 288 LRTGLMGIFSLCMLPFLANVLRALVGPSPVSGVFIALNMLGYANSAFNPLIY-CRS 34

QY 346 RQIRGELSKQFVCFKPAPEELR-----LPSREGIEENLQFLQCNCPSESWVS 39

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Db 347 P D F R L L C S Y G R G P E E R V V T F P A S P V A S R Q N S P L N R F ----- D G Y E G E ----- 39

```

QY 398 RPLPS 402

Db 396 RFPPT 400

RESULT 9

A41679

beta-3-adrenergic receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 13-Aug-1999

C:Accession: A41679

R:Muzin, P.; Revelli, J.P.; Kuhne, F.; Gocayne, J.D.; McCombie, W.R.; Venter, J.C.; Gil

A:Title: An adipose tissue-specific beta-adrenergic receptor. Molecular cloning and down

A:Reference number: A41679; MUID:92084710; PMID:1721063

A:Accession: A41679

A:Molecule type: mRNA

A:Residues: 1-400 <M2>

A:Cross-references: GB:M74716; NID:9950087; PIDN:AAA4470.1; PID:g202766

A:Experimental source: Brown adipose tissue

A:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 336; DB 2; Length 400;

Best Local Similarity 28.2%; Pred. No. 1.2e-19;

Matches 120; Conservative 64; Mismatches 189; Indels 52; Gaps 17;

QY 4 SPIPGNSSTLGRVPO-TPGSTAGVPEVGLRDVASEGVAFEMILLDTAVAGNAA 62

Db 2 APMPHKGSLAFMSDAPTLDPSSAANTSGLPV-----PMAALLAGALLALATVGGNLL 54

QY 63 VMAVIATPALRKF-VFVHICLVLDLALTLPLMLSSSALFDHALFGEVACRLYLF 120

Db 55 VIVAIARTPLQITNTNFVTSLATADLVGLLVMPG-ATLALTGHPGLGATGCELTMS 112

QY 121 LSVCFVSLATLSAIVERYVYVHPMKREVRMTGLVASLVGVWVKALAMASVPLG 180

Db 113 VDVLCTVASTETCALAVDRLATVNLPLRGTLTKRRARAVALVWVTSVTFAPFMS 172

QY 181 RVSMEEGAPSVPPGCSLQMSHAYCOL-----FVYFAVLFLPLLLIIVVYCSMFYVA 235

Db 173 Q-WMRVGADAEAOCH---SNPRCCSFASNMRYALLSSVSFYPLVLMFLVYARVYVA 228

QY 236 ----RVAMOHGPLPTMMEPR--ORSESLSSRSTWMTSSGAPQ--TTPHR--TFGGGKA 285

Db 229 KRRRFRRRELGRPP--EESPRSPSPSPATVGTPTASDGPSCGRPARLLPLGEHRA 287

QY 286 AVVLAVGGOFLLCMLPYFSFHLVVALSAQISTGOVESVWTWIGYCFSTNPFYGCIN 345

Db 288 LRTGLTGMGIFSLCMLPFPLANVRLALVGPLVSGVFIALNMLGYNASAFNPPLY-CRS 346

QY 346 RQIRGELSKQVCFKPAPEELR-----LPSREGSIEENFLQFLOGTGCPSSESVVS 397

Db 347 PDPR-DAPFRLLCSYGGRCPEPRVYTFPASVVASRONSPLNRF-----DGYEGE---- 395

QY 398 RPLPS 402

Db 396 RPFPT 400

RESULT 10

S65459

beta-3-adrenergic receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999

C:Accession: S65459; S40504; S31659

R:Pietri-Roussel, F.; Lenzén, G.; Kapoor, A.; Drumare, M.F.; Archimbaud, P.; Strosberg,

Eur. J. Biochem. 230, 350-358, 1995

A:Title: Molecular cloning and pharmacological characterization of the bovine beta3-adre

A:Reference number: S65459; MUID:95324546; PMID:7601122

A:Accession: S65459

A:Molecule type: mRNA

A:Residues: 1-405 <PE>

A:Cross-references: EMBL:X85961; NID:9757758; PIDN:CAA59937.1; PID:9757759

A:Experimental source: Brown adipose tissue

R:Castella, L.; Muzin, P.; Revelli, J.P.; Ricquier, D.; Giacobino, J.P.

Biochem. J. 297, 93-97, 1994

A:Title: Expression of beta(1)- and beta(3)-adrenergic-receptor messages and adenylylat

ite fat.

A:Reference number: S40503; MUID:94107292; PMID:7904157

A:Accession: S40504

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 162-298 <CAS>

R:Stoffel, B.; Meyer, H.H.D.

Submitted to the EMBL Data Library, June 1992

A:Description: Bovine beta3-adrenergic receptor, partial genomic sequence.

A:Reference number: S31659

A:Accession: S31659

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 4-5, 'HE', 8-105 <STO>

A:Cross-references: EMBL:X67214

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran

F:73-63/Domain: transmembrane #status predicted <TM1>

F:73-101/Domain: transmembrane #status predicted <TM2>

F:113-133/Domain: transmembrane #status predicted <TM3>

F:156-179/Domain: transmembrane #status predicted <TM4>

F:204-225/Domain: transmembrane #status predicted <TM5>

F:293-314/Domain: transmembrane #status predicted <TM6>

F:327-347/Domain: transmembrane #status predicted <TM7>

F:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 335.5; DB 2; Length 405;

Best Local Similarity 28.1%; Pred. No. 1.3e-19;

Matches 121; Conservative 67; Mismatches 183; Indels 59; Gaps 18;

QY 7 POSSGNSSTLGRVQTP-GRST--ASGVPEVGLRDVASEGVAFEMILLDTAVAGNAA 62

Db 3 PMPGNSG-LTPWDPITPLAPNTANASGLPVPW---AVALLAGALLALAVLAVGGNLL 57

QY 63 VMAVIATPALRKF-VFVHICLVLDLALTLPLMLSSSALFDHALFGEVACRLYLF 120

Db 58 VIVAIARTPLQITNTNFVTSLATADLVGLLVPPG-ATLALTGHPGLGATGCELTMS 115

QY 121 LSVCFVSLATLSAIVERYVYVHPMKREVRMTGLVASLVGVWVKALAMASVPLG 180

Db 116 VDVLCTVASTETCALAVDRLATVNLPLRGALVTKRRALAVALVWVTSVTFAPFMS 175

QY 181 RVSMEEGAPSVPPGCSLQMSHAYCOL-----FVYFAVLFLPLLLIIVVYCSMFYVA 235

Db 176 K-WMRIGADAEAOCH---SNPRCCTFASNMRYALLSSVSFYPLVLMFLVYARVYVA 231

QY 236 ----RVAMOHGPLPTMMEPR--ORSESLSSRSTWMTSSGAPQ--TTPHR--TFGGGKA 285

Db 232 TRQIRLRLRELGRPPPEESPPAPRSQSPGLAGCASAGVPSGRPARLLPLREH--- 288

QY 284 KAAVVLAVGGOFLLCMLPYFSFHLVVALSAQISTGOVESVWTWIGYCFSTNPFYGC 343

Db 289 RALRTGLTGMGIFSLCMLPFPLANVRLALVGPLVSGVFIALNMLGYNASAFNPPLY-C 347

QY 344 LNRQIRGELSKQVCFKPAPEELR--PSREGSIEENFLQFLOGTGCPSSESVSRPL 401

Db 348 RSPDERSAF-RRLC--RCRPEEHLAASPPR-----APGAPATALTSP 388

QY 402 SPKQPPAVD 411

Db 389 AGPWQPELD 398

RESULT 11

A55044

beta-4c-adrenergic receptor - turkey

C:Species: Meleagris gallipavo (common turkey)

C>Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C:Accession: A55044

R:Chen, X.; Harden, T.K.; Nicholas, R.A.

J. Biol. Chem. 269, 24810-24819, 1994

A:Title: Molecular cloning and characterization of a novel beta-adrenergic receptor.

A:Reference number: A55044; MUID:95014249; PMID:7929160
A:Accession: A55044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <CH>
A:Cross-D-references: GB:U13978; NID:9555881; PIDN:AAA62151.1; PID:9555882
C:Genetics:
A:Introns: 416/2
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor; transmembrane protein

Query Match 14.5% Score 335; DB 2; Length 428;
Best Local Similarity 27.3% Pred. No. 1,5e-19;
Matches 115; Conservative 59; Mismatches 179; Indels 68; Gaps 15;

QY 22 TPGPSTASGVPEVGLRDVASEVALFEMLLD-LTVAGNAAMVIAKTPALRKF--VF 78
DB 2 TPLPAGNSVPCNSMAAVLSROMAVGALSTITLIVAGNLLIVIAIAKTPRLQGTWTF 61
QY 79 VFHLCLVDLLAALTLMPMLAMSSALFDHALFGEVACNLYFLSCFVSLAISVAINV 138
DB 62 VYSLACADLVMGILLVPPG--ATILLGHPYGTVCCELMSLDVLCVYASITETLCIAIV 119
QY 139 ERYVVVHPREYERMLGLVASYLVGVVWKAAMASVPVLGRVSMEGAPSPVPCSLQ 198
DB 120 DRLATLAPLQYELALYTKGRAMAVVCWMAISAFISFLPINNH-WRRQADAEQAVNC--- 175
QY 199 WSHSAYCOL-----FVVVFAVLVFLRLDLLLVYCSNFRVA-----RVAAMQHG 243
DB 176 YDDPRCCDFVTNMTYALVSSVSFYVPLVMIIFYVAVVAVATRVHQLGKDKVRLQEN 235
QY 244 PLPTMETPRQSESSLSRSMTWSSGAPOTTPIHRTG--GGAAYVLLAVGGQFLCWL 301
DB 236 P-----SLSSR-----GGRMRPRSLIAIKERKALKTLGIIINGTFLCWL 275
QY 302 PYGFFLLVYALASQPISTGQVESVYTWIGYFCFINSPPFYGLNRQIRGSLKQFQCFPK 361
DB 276 PEFVANI-IVFCRPLVDDQLFLFLNMLGYNSAFNPITY-CRSPDFSAFKRLCC--- 330
QY 362 PAPEELRLPQRSSESLDENLQFLQGTCCPSESWSRPLSPSPKPPADFRIPQIAEE 421
DB 331 -----PRADRLRHAAAPQDPQHCSC-----AFSPRGDMESKAVD---PGHLRED 373
QY 422 T 422
DB 374 S 374

RESULT 12
139369
alpha-1A-adrenergic receptor - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 13-Aug-1999
C:Accession: I39369; J02331
R:Esbenstade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Mineman, K.P.; M
Mol. Pharmacol. 47, 977-985, 1995
A:Title: Cloning of the human alpha-1A-adrenergic receptor and inducible expression of t
A:Reference number: I39369; MUID:95265059; PMID:7746284
A:Accession: I39369
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-572 <RES>
A:Cross-D-references: GB:D29952; NID:9914933; PIDN:BAA06222.1; PID:9914934
R:Meinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitor, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A:Title: Cloning, expression and characterization of human alpha adrenergic receptors al
A:Reference number: J02331; MUID:94296402; PMID:8024574
A:Accession: J02331
A:Molecule type: mRNA
A:Residues: 1-30, 'G', 32-521, 'P', 523-572 <MET>
A:Note: the authors translated the codon CCC for residue 522 as Arg
C:Genetics:
A:Gene: GDB:ADRA1A; ADRA1; ADRAIR

A:Cross-references: GDB:118749; OMIM:104219
A:Map position: 20pter-20qter
A:Introns: 37/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:89-123/Domain: transmembrane #status predicted <TM1>
F:132-163/Domain: transmembrane #status predicted <TM2>
F:172-197/Domain: transmembrane #status predicted <TM3>
F:208-235/Domain: transmembrane #status predicted <TM4>
F:254-278/Domain: transmembrane #status predicted <TM5>
F:344-374/Domain: transmembrane #status predicted <TM6>
F:380-414/Domain: transmembrane #status predicted <TM7>
F:65,82/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 332.5; DB 2; Length 572;
Best Local Similarity 24.2%; Pred.No. 3,3e-19;
Matches 122; Conservative 77; Mismatches 204; Indels 101; Gaps 16;

QY 12 NSTSLGRVOTGTPSTASGVPEGLRDVASSEAL-FEMLLDLTAVAGAAVAIAKT 70
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 65 NSSSAEPPGSAGAGDGNNTAAAGLVLSAQGGVGVELFAFLTMAAGMLIVLSPACN 124

QY 71 PALRKFEV--FVFHLCVDLTALTLPLAMLSAALFDHALFGVCARLTFVSVPVL 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 125 RHLOQTYNFTIYNLAADILLSTVLPFS--ATMEVLGFAGFRACDVAAADVLCCTA 182

QY 129 AILSVSAINVERYYVVVHPMRVEVRMTLGIVASLVGVWVKALAMASVPYLGRYSMEGA 188
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 183 SILSCTISVDRYGVGRHSILKYPAIMTERKKAAILALLMWVALVSVGPLG--WKE-- 237

QY 189 PSVPPGCSLOWSHSATCOL-----FYVFAVLFTLLPLLILVYSCMFVAR--VAAMQ 241
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 238 -FVPP-----DERCGITIEAGYAVFSSCFYIPMAIYVMYCIVVYVARSTRSLE 289

QY 242 HPRPLPTMETPQRORS-----LSSRSTMVTSSG--PQTPTPHRTPGCG----- 283
Db 290 AG-----VKREGKASEVVLRIHQRAATGADGAKHGMSAKGHTRSSLVRLKFSR 342

QY 284 --KAANVLLAVSGOEFKLCLWPFSFHLVVALSAQPISTGCVESVVMWIGCYCTSNPFY 341
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 343 EKKAKKTIALIVGVFLICMPFFPVLPGLSLPQLRPSEGVFVIMLGIFFNSCVNPILI 402

QY 342 GCLNLINGELSKQFYCCFK-----PAPEELRLDSREGSIDENLQFL 385
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 403 PCSSREFKRAFRLRLQCRRRRRRRLRVVGHMHRASTGLROCAPSS----- 453

QY 386 OGTCGPESSEWWRPLPSKPQEPRAV-----DFRPGIABETSFFLE 427
Db 454 -GDAPRGAPLAIPLDPDEPPPGTPREMOAPVASRRKPPSAFREWRLGFRPRTT--- 508

QY 428 QOLTSDIIMSDSLPRPASPRLES 451
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 509 -QLRAKVSSLSHKIRAGGAORAEA 531

RESULT 13
157942
5-hydroxytryptamine receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I57942
R:Monsma, F.J.
MOL.Pharmacol. 43, 320-327, 1993
A>Title: Cloning and expression of a novel serotonin receptor with high affinity for
A:Reference number: I57942; MUID:93196608; PMID:7680751
A:Accession: I57942
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-437 <RES>
A:Cross-references: GB:I03202; NID:g294507; PIDN:AAA0618.1; PID:g294508
C:Superfamily: vertebrate rhodopsin

Query Match 14.2%; Score 329.5; DB 2; Length 437;

Best Local Similarity 27.3%; Pred. No. 4.3e-19;
Matches 128; Conservative 65; Mismatches 181; Indels 95; Gaps 19;

QY 2 ESSPIPOSSNSSTLGRVPOTPGPSTASGVPEVGLRDVASESVALFPMILLDLTAVAGNA 61
D 4 EEPVP-----NSST-----PAMGPPPPAPG-----GSGWMAALCVIYVLA--AANS 45
QY 62 AVAAVIAKPPALRKF--VFVHLCIVDILAALTMLPLMSSSAFDHALFGEVACRLYL 119
D 46 LILVILCTOPAVRNNTSNFVLVSLFTSDLMGLVMPAPML--NALYGRWVLANGCLLMT 103
QY 120 FLSCFVSLATLSVAIINVERYYVHPMRYEVRMTLGLVASVLGVWVKALAMASVPLG 179
D 104 APDVNCCASILNLCILSDRIYLLISPLRYKLRMTAPRALIILGMSLAALASFLPL 163
QY 180 GRVSWEB--GAPVSP--PCCSLQWMSHAYCOL-----FVYFAVLYFLLPLLLLVYCSMF 232
D 164 --LGMHELGRKAPTPAG-----QCRLASLPEVLVAGVTFPLPSGALCFYTCRIL 212
QY 233 RVARVAMQHGRLPTWM-----ETPRQSESLSRSTMVYSSGAPQTPPHRTFG 281
D 213 LAARKAOVVOVASLTTGTAGALETLQVPRTPRGOMESADSRRLATKHSRAL----- 264
QY 282 GCAAAVLLAVGQFLCMLPYFSFHLVYALSAQPISTGVESVYTWIGFCFTSNPFY 341
D 265 --KASLTGLGLGMFFWTMLPFVAVNIAQAV--CDCISPLGLFD--VLTMLGVCNSTMPNIIY 320
QY 342 GCLNROIIGELSKQFV-----CFKPAPEELRLP-----S 372
D 321 PLTFPRFKRALGR--FLHASTVPRSTGCPCLPLHVDLSQRCQTRPQLQOVALPLPNSDS 379
QY 373 RESSIEENFLQFLOGTGPCSESWNSRPLPSPKQEPAPVADRIGQIAEE 421
D 380 DSASGCTSGIQLTAQLLPGEA--TRDPPPTATTAVNEFVDSVEPE 426

RESULT 14

S32804

beta-3-adrenergic receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 13-Aug-1999

C:Accession: S32804; S32827; S18548

R:Emorine, L.J.

submitted to the EMBL Data Library, March 1993

A:Reference number: S32803

A:Accession: S32804

A:Molecule type: DNA

A:Residues: 1-400 <EMO>

A:Cross-references: EMBL:X72862; NID:q298112; PIDN:CAA51384.1; PID:q298113

R:van Spronsen, A.; Nahmias, C.; Krief, S.; Briand-Sutren, M.M.; Strosberg, A.D.; Emorin

Eur. J. Biochem. 213, 1117-1124, 1993

A:Title: The promoter and intron/exon structure of the human and mouse beta3-adrenergic-

A:Reference number: S32826; MUID:93279311; PMID:8389293

A:Accession: S32827

A:Molecule type: DNA

A:Residues: 1-8; 341-347; 380-400 <SPR>

A:Cross-references: EMBL:X60438; NID:q50109; PIDN:CAA42966.1; PID:q50110

A:Residues: 1-388 <NAH>

C:Genetics:

A:Map position: 8A2-4

A:Introns: 388/2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

F:37-60/Domain: transmembrane #status predicted <TM1>

F:70-88/Domain: transmembrane #status predicted <TM2>

F:110-130/Domain: transmembrane #status predicted <TM3>

F:153-176/Domain: transmembrane #status predicted <TM4>

F:201-222/Domain: transmembrane #status predicted <TM5>
F:320-311/Domain: transmembrane #status predicted <TM6>
F:324-344/Domain: transmembrane #status predicted <TM7>
F:8;26/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 14.1%; Score 326.5; DB 2; Length 400;
Best Local Similarity 27.4%; Pred. No. 6.8e-19;
Matches 107; Conservative 61; Mismatches 171; Indels 51; Gaps 12;

QY 4 SPIPOSSNSSTLGRVPO--TPGPSTASGVPEVGLRDVASESVALFPMILLDLTAVAGNA 62
D 2 APVHRNGSLALMSDAPTLDPASAANTSGLPV-----PMAALAGALLATATVGNLL 54
QY 63 VMAVIAKPPALRKF--VFVHLCIVDILAALTMLPLMSSSAFDHALFGEVACRLYL 120
D 55 VILAIARTPLRLQTTNVTNVSLLAAADLVGLLVNPPG--ATLALTGMHPIGEGCELTMTS 112
QY 121 LSCFVSLATLSVAIINVERYYVHPMRYEVRMTLGLVASVLGVWVKALAMASVPLG 180
D 113 VDYLCTVASIETICALAVDRILAVTNPLRGTLYTKRARAAYLVNIVSAVSFAFIMS 172
QY 181 RVSWEGAPSVPPCCSLQWMSHAYCOL-----FVYFAVLYFLLPLLLLVYCSMPRVA 235
D 173 Q--WRVGADEAEOCH--SNPRCCSPASNPYALLSSVSFYLLVLMFVYARFVVA 228
QY 236 -----RVAAHQHGRLPTWMETPRQSESLSRSTMVYSSGAP-----QTP 276
D 229 KROHLLRELGRFSPESPSPS-----RSPSPATGGPAPADVPVCGRRAPALPL 281
QY 277 HRTFGGKAADVLLAVGQFLCMLPYFSFHLVYALSAQPISTGVESVYTWIGFCFTS 336
D 282 LREH--RALRTGLMGITSLCMLPFFLVNLRALAGPSLVPESGVETALNMWIGYANSF 338
QY 337 NPFYGLNROIIGELSKQFVCFKPAPEE 366
D 339 NPVIY--CRSPDFRDAFRRLLCSTYGRGPEE 367

RESULT 15

ORH0B3

beta-3-adrenergic receptor, splice form 2 - human

N:Alternate names: beta-3-adrenergic receptor form A

C:Contains: beta-3-adrenergic receptor splice form 1

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 16-Jun-2000

C:Accession: A41348; S33752

R:Emorine, L.J.; Marullo, S.; Briand-Sutren, M.M.; Patey, G.; Tate, K.; Delavier-Klut

Science 245, 1118-1121, 1989

A:Title: Molecular characterization of the human beta-3-adrenergic receptor.

A:Reference number: A41348; MUID:89368947; PMID:2570461

A:Accession: A41348

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-402 <EMO>

A:Cross-references: GB:M29932; NID:q178895; PIDN:AAA3550.1; PID:q178896

A>Note: splice form 1

R:Leblais, J.M.; Kagnad, M.; Rodriguez, M.; Chalon, P.; Bonnin, J.; Dupre, I.; Delpech

FEBS Lett. 324, 127-130, 1993

A:Title: Molecular cloning of a human beta-3-adrenergic receptor cDNA.

A:Reference number: S33751; MUID:93285320; PMID:8389717

A:Accession: S33752

A:Molecule type: DNA

A:Residues: 392-414 <LEL>

A:Cross-references: EMBL:X70812; NID:q312398; PIDN:CAA50142.1; PID:q1666375

A>Note: splice form 2

C:Genetics:

A:Gene: GDB:ADRB3

A:Cross-references: GDB:203869; OMIM:109691

A:Map position: 8p12-8p11.1

A:Introns: 402/2

C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane

F:1-414/Product: beta-3-adrenergic receptor precursor splice form 2 #status predicted

F.1-402/Product	beta-3-adrenergic receptor precursor	splice form 1	status predicted <
F.37-63/Domain	transmembrane	status predicted <TM1>	
F.73-101/Domain	transmembrane	status predicted <TM2>	
F.113-133/Domain	transmembrane	status predicted <TM3>	
F.156-178/Domain	transmembrane	status predicted <TM4>	
F.204-225/Domain	transmembrane	status predicted <TM5>	
F.293-314/Domain	transmembrane	status predicted <TM6>	
F.327-341/Domain	transmembrane	status predicted <TM7>	
F.8-26/Binding site	carbohydrate (Asn)	(covalent)	status predicted

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OM protein - protein search, using sw model

Run on: December 10, 2002, 09:56:35 : Search time 18 Seconds
(without alignments)
737.208 Million cell updates/sec

Title: US-09-838-028-2

Sequence: 1 MESSPIRQSSGNSSTLGRVP.....SDIRMSDYLRPASPRLES 451

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued_Patents_AA:*
1: /cgn2_6/prodata1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	1276	55.0	252	3	US-08-513-974B-52
2	1276	55.0	252	3	US-08-513-974B-360
3	351	15.1	358	2	US-08-748-485-6
4	350	15.1	359	2	US-08-103-170-7
5	349	15.1	359	1	US-07-996-772A-10
6	349	15.1	359	2	US-08-748-485-3
7	349	15.1	359	4	US-09-328-314-19
8	347	15.0	348	4	US-08-875-540-13
9	347	15.0	348	4	US-09-171-456-17
10	347	15.0	348	4	US-09-473-634-13
11	346	14.9	359	2	US-08-103-170-4
12	346	14.9	359	2	US-08-103-170-6
13	343	14.8	359	2	US-08-748-485-5
14	340	14.7	359	2	US-08-467-568-13
15	340	14.7	359	2	US-08-748-485-4
16	340	14.7	359	2	US-08-103-170-2
17	340	14.7	359	2	US-09-030-582-13
18	340	14.7	359	3	US-08-875-540-15
19	340	14.7	359	4	US-09-171-456-19
20	340	14.7	359	4	US-09-473-634-15
21	337	14.5	400	1	US-07-916-901-6
22	336	14.5	400	1	US-07-783-602C-1
23	335.5	14.5	405	1	US-08-351-473B-2
24	335	14.5	400	1	US-08-351-473B-4
25	332.5	14.3	572	1	US-08-354-698-2
26	332.5	14.3	572	1	US-08-228-932-2
27	332.5	14.3	572	1	US-08-468-939-2

28	332.5	14.3	572	1	US-08-722-001-30	Sequence 30, App1
29	332.5	14.3	572	2	US-08-406-855A-2	Sequence 2, App1
30	332.5	14.3	572	3	US-08-722-190-2	Sequence 2, App1
31	332.5	14.3	572	3	US-08-244-354-2	Sequence 2, App1
32	332.5	14.3	572	3	US-09-206-899-2	Sequence 2, App1
33	332.5	14.3	572	4	US-09-444-783-2	Sequence 2, App1
34	332.5	14.3	572	4	US-09-688-415-7	Sequence 2, App1
35	332.5	14.3	572	5	PCT-US95-04203-2	Sequence 2, App1
36	326.5	14.1	368	1	US-08-087-772A-2	Sequence 2, App1
37	326.5	14.1	400	1	US-08-351-473B-5	Sequence 5, App1
38	326.5	14.1	400	4	US-08-450-962-4	Sequence 4, App1
39	326.5	14.1	400	4	US-08-450-962-6	Sequence 6, App1
40	325	14.0	501	4	US-09-688-415-7	Sequence 7, App1
41	322.5	13.9	560	4	US-09-688-415-8	Sequence 8, App1
42	321	13.8	559	2	US-08-406-855A-20	Sequence 20, App1
43	321	13.8	559	3	US-09-206-899-20	Sequence 20, App1
44	320	13.8	501	1	US-08-722-001-14	Sequence 14, App1
45	320	13.8	501	2	US-08-467-568-9	Sequence 9, App1

ALIGNMENTS

RESULT 1
US-08-513-974B-52
: Sequence 52, Application US/08513974B
: Patent No. 6114139
: GENERAL INFORMATION:
: APPLICANT: Hinuma, Shuji
: APPLICANT: Hosoya, Masaki
: APPLICANT: Fujii, Ryo
: APPLICANT: Ohtaki, Tetsuya
: APPLICANT: Fukusumi, Shoji
: TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
: TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
: NUMBER OF SEQUENCES: 380
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
: STREET: 130 Water Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: FILING DATE: 14-SEP-1995
: APPLICATION NUMBER: US/08/513,974B
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP95/01599
: FILING DATE: 10-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-093989
: FILING DATE: 19-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-057186
: FILING DATE: 16-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-007177
: FILING DATE: 20-JAN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-326611
: FILING DATE: 28-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-270017
: FILING DATE: 02-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236357

FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-52

Query Match 55.0%; Score 1276; DB 3; Length 252;
Best Local Similarity 98.0%; Pred. No. 1,9e-92;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 VDLAALTLPMLMSSALFDHALGFEVACRLYLPLSVCFSLATISVAINVERYYV 144
DB 1 VDLAALTLPMLMSSALFDHALGFEVACRLYLPLSVCFSLATISVAINVERYYV 60
QY 145 VHMREYVRMTGLVAVSVLVGVVWKALAMASVPLGRVSEEGAPSVPCGSIQMSHSAY 204
DB 61 VHMREYVRMTGLVAVSVLVGVVWKALAMASVPLGRVSEEGAPSVPCGSIQMSHSAY 120
QY 205 COLFYVFAVLYFLPLLLLVYCSMFRAVAAOMHGFLPTWETPRORSELSRSRT 264
DB 121 COLFYVFAVLYFLPLLLLVYCSMFRAVAAOMHGFLPTWETPRORSELSRSRT 180
QY 265 MWTSSGAPOTTPTRTGGKAAVLLAVGGOFLLCMLPYSPFHLVYALSQPISTGQVES 324
DB 181 MWTSSGAPOTTPTRTGGKAAVLLAVGGOFLLCMLPYSPFHLVYALSQPISTGQVES 240
QY 325 VVTWIGYFCFTS 336
DB 241 VVTWIGYFCFTS 252

RESULT 2
US-08-513-974B-360
Sequence 360, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-974B-360

Query Match 55.0%; Score 1276; DB 3; Length 252;
Best Local Similarity 98.0%; Pred. No. 1,9e-92;
Matches 247; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 VDLAALTLPMLMSSALFDHALGFEVACRLYLPLSVCFSLATISVAINVERYYV 144
DB 1 VDLAALTLPMLMSSALFDHALGFEVACRLYLPLSVCFSLATISVAINVERYYV 60
QY 145 VHMREYVRMTGLVAVSVLVGVVWKALAMASVPLGRVSEEGAPSVPCGSIQMSHSAY 204
DB 61 VHMREYVRMTGLVAVSVLVGVVWKALAMASVPLGRVSEEGAPSVPCGSIQMSHSAY 120
QY 205 COLFYVFAVLYFLPLLLLVYCSMFRAVAAOMHGFLPTWETPRORSELSRSRT 264

Db 121 COLFVVFVAVLYFLPLLLILVYCSMFVRVAVAMQHCPPTWMTETPRORSESLSSRST 180
Qy 265 MTSSGAPQTPHRTFGGKAAYVLLAVGGFLLCMLPYFSEPHLYVALSAQPISTGQVES 324
Db 181 MTSSGAPQTPHRTFGGKAAYVLLAVGGFLLCMLPYFSEPHLYVALSAQPIAGOVEN 240
Qy 325 VVTWIGVECFETS 336
Db 241 VVTWIGVECFETS 252

RESULT 3
US-08-748-485-6
; Sequence 6, Application US/08748485
; Patent No. 5817480
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Goll, Surya K.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,485
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0159 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 236184
; US-08-748-485-6

Query Match 15.1%; Score 351; DB 2; Length 358;
Best Local Similarity 27.5%; Pred. No. 5e-20;
Matches 106; Conservative 58; Mismatches 150; Indels 72; Gaps 12;

Qy 43 SVALFMLLDLTAVAGNAAMAVIAKTPALRKFFV--FVPHLCIVDLALATLMLPLAMLS 100
Db 22 SVVLTTLTLI--TLAGVNVVCLAVSLNRRLSLTNCITVSLAATDILLGLVLPF---- 74
Qy 101 SSALEFDNAL---FGEVACRLYLFLSVCFVSLAIVSAIINVERRYVVVPHMKREYRMGL 157
Db 75 -SAIYOLSFVTSFGHVFECNITVSLDVMCTASINLTFMISIDRYCAVAVDPLRPVLYPV 133
Qy 158 LVASVLGVVWVKALAMASVPLVIGRVSMEE-----GAPSVFPGCSLQMSHAYQCLFFVV 211

Db 134 RVALSLVETWISTLSLST--HGMVSRNGTRGNGNFTK--CKVQYN-----EVLGLV 184
Qy 212 FAVLYFLPLLLILVYCSMFVRVAVAMQHCPPTWMTETPRORSESLSSSTWYSSGA 271
Db 185 DGLVTFYFLPLIMCVTYRIKFIAREQAKRINHISMMKAA----- 224
Qy 272 POTPHRTFGGKAAYVLLAVGGFLLCMLPYFSEPHLYVALSAQPISTGQVESVYTWIGY 331
Db 225 -----TIREHKATVTLAAVGAFTICWPFYFAVYRGLRGDDAINEAVEGIVLWLG 277
Qy 332 FCFSTNPFYGCINRQINGELSKOFVCFKP--APEELRL-----PSREGISEENF 381
Db 278 ANSALNPLIYALALNDRPFTAAQQLFHCKFASHNSHKTSLRLNLSLPSQSREGWQDEK 337
Qy 382 LQFLOGTGCPSSESVSRPLPSPKQEP 407
Db 338 PLKIQ-----VMSGTELTHPQGNP 356

RESULT 4
US-08-103-170-7
; Sequence 7, Application US/08103170
; Patent No. 5885824
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantiz, Ita
; TITLE OF INVENTION: Recombinant Genomic Clones Encoding
; TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, Methods for Production
; TITLE OF INVENTION: Thereof, and Proteins Encoded Therefrom
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/103,170
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/633,060
; FILING DATE: 24-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallee, Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-017-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 24885 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; IMMEDIATE SOURCE:
; ORGANISM: Dog
; US-08-103-170-7

Query Match 15.1%; Score 350; DB 2; Length 359;
Best Local Similarity 28.7%; Pred. No. 6e-20;
Matches 100; Conservative 56; Mismatches 140; Indels 52; Gaps 10;

```

Oy 3VALFEMFLDLDTLVAGAAVAAMVIAATPAIRKVP--FVFLICVDLAAATLTPMLAMS 100
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 22SVLTVLTLI---TIAGVAVVCLAVGNRRRLRSLTNCFIYSLATIDLLGLVLFP---- 74
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Oy 101SSALFDNAL---PEEVACRLYLELVSCEVSLAISVSHINERYVYVHPRREVRMTLG 157
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 75-SAFYQUSCRMSFFKVFCONITSLDVMICLASISLNFEMISIDRCATVDPRLPVLLTPV 133
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Oy 158LVASIVGVWVKALAMASVPV-LGRVSMEEGAP--SVPPGSLQMSHSACQLFVVVFAV 214
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 134RVAVSLVLIWVITSLPSLTLHLCMNSTNENSSFNHITPCKQVYV-----LVYGLVDGL 188
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Oy 215LYFLPLLLLLIYVYCSMPRVARVAAMOHGRLPTMETPRQROSESLSRSTWVYSSGAPQT 274
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 189VTFPLPLLLVMTIYTRFLKPIARDADAKRIHHGSKAA----- 225
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Oy 275TPHRTFGGGAANVLLVAVGGQFLCMLPYESFNHLYVVALSQIPSTGQVESVYTWIGYCF 334
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 226----TIGEHKATVTLAAVMGAFFIICMPPEYTFVYRGKGGDDALINEAFVAVMLGVANS 281
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Oy 335TSNPFYCCCLROTRGELSKRQVCFKPARP--DELALPREGSIEEN 380
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 282ALNPLVLTATLNDRFTAYQQLPFC--PRASINAEOTELRSNSOLLARN 327
    || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

```

```

: RESULT 5
: US-07-996-772A-10
: Sequence 10, Application US/07996772A
: Patent No. 5472866
: GENERAL INFORMATION:
: APPLICANT: Gerald, Christophe
: APPLICANT: Hartig, Paul R.
: APPLICANT: Brancheau, Theresa A.
: APPLICANT: Weinschenk, Richard L.
: TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN
: TITLE OF INVENTION: RECEPTORS AND USES THEREOF
: NUMBER OF SEQUENCES: 12
: CORRESPONDING ADDRESS:
: ADDRESSEE: COOPER & DUNHAM
: STREET: 30 ROCKEFELLER PLAZA
: CITY: NEW YORK
: STATE: NEW YORK
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/996,772A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, P., John
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 42667/JPW/TEP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 977-9550
: TELEFAX: (212) 664-0525
: TELEX: 422523 COOP UT
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 359 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IMMEDIATE SOURCE:
: CLONE: HIF2
: US-07-996-772A-10
:
: Query Match 15.1%; Score 349; DB 1; Length 359
: Best Local Similarity 28.7%; Pred. No. 7; le-20;

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[illegible]

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1  RESULT 6
2  US-08-748-485-3
3  Sequence 3, Application US/08748485
4  Patent No. 5811480
5  GENERAL INFORMATION:
6  APPLICANT: Au-Young, Janice
7  APPLICANT: Gueglert, Karl J.
8  APPLICANT: Goli, Suyu K.
9  APPLICANT: Murry, Lynn E.
10 TITLE OF INVENTION: NOVEL HISTAMINE H
11 NUMBER OF SEQUENCES: 8
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: INCYTE PHARMACEUTICALS,
14 STREET: 3174 Porter Drive
15 CITY: Palo Alto
16 STATE: CA
17 COUNTRY: US
18 ZIP: 94304
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Diskette
21 COMPUTER: IBM Compatible
22 OPERATING SYSTEM: DOS
23 SOFTWARE: FASTSEQ Version 2.0
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/748,485
26 FILING DATE: Herewith
27 CLASSIFICATION: 530
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:
30 FILING DATE:
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Billings, Lucy J.
33 REGISTRATION NUMBER: 36,749
34 REFERENCE/DOCKET NUMBER: PF-0159 US
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 415-855-0555
37 TELEFAX: 415-845-4166
38 TELEX:
39 INFORMATION FOR SEQ. ID NO: 3:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 359 amino acids
42 TYPE: amino acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 IMMEDIATE SOURCE:
46 LIBRARY: GenBank

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; Patent No. 6346380
; GENERAL INFORMATION:
; APPLICANT: Wright, Simon Ralph
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; TITLE OF INVENTION: DETECTION OF VARIATIONS IN HUMAN H2 RECEPTORS
; FILE REFERENCE: 09347/004001
; CURRENT APPLICATION NUMBER: US/09/171,456A
; EARLIER FILING DATE: 1999-08-03
; EARLIER APPLICATION NUMBER: PCT/GB97/01075
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-171-456-17

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Query Match          15.0%: Score 347; DB 4; Length 348;
Best Local Similarity 28.6%: Pred. No. 9.9e-20;
Matches 99; Conservative 57; Mismatches 132; Indels 58; Gaps 10;

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QY 49 MLLDLTAVAGNAVMVIAKTPALRKRV--FVPHCLVDLALTLMPMLSSALFD 106
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DB 22 LAVILITVAGNVVCLAVGLNRRLNLTNCFIVSLAITDLLGLVLPF-----SAITYQ 76
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 107 HAL---FGEVACRLYLELSCVFSALISVAINVERIYVYVHMRREVRTGLVASVL 163
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 77 LSCWMSGKVCFCNITSLDVMCLTASILNLFMISLDRCVAMDLRVPVLTTPARVAISL 136
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 164 VGWVVKALAMASVPV-LGRVSWMEGAPS--VPPGCSLQWSHSAVCQLFVYVFAVLFLP 220
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 137 VLIWVISTITLSFLSIHGLMNSRNKTSKGNHTTSKCNQVN-----EYGLVDGLVTFELP 191
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 221 LLLILVYCSMFRAVRAVAAOHGFLPTWMETPRQRSELSRSTMTVSSGAPQTPTRTF 280
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 192 LLIMCITYRIFRVARQAKRIDHSSWK-----AATIREHR-- 228
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 281 GCGKAAYVLLAVGQFLCMLPFPSFHLVYVALSAQPISTGQVESVWIGFCTSPNPF 340
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 229 ---ATVTLAAVMGAFITICMPYFTAFVYRGLRGDDAINEMLEAIVMLGYANSALNPIL 284
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 341 YGCLNROI RGLSKQFCFKPAPEELRLPSREG---SIEENFLQ 383
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 285 YAALNRDFRTGYQQLFCC-----RLANRSHKTSLSRNSAQ 320
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

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RESULT 10
US-09-473-634-13
; Sequence 13, Application US/09473634
; Patent No. 6440670
; GENERAL INFORMATION:
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; APPLICANT: Wright, Simon Ralph
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
; FILE REFERENCE: 09347/002001
; CURRENT APPLICATION NUMBER: US/09/473, 634
; CURRENT FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 08/875, 540
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: PCT/EP96/00397
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: GB9503866.7
; PRIOR FILING DATE: 1995-01-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 348

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-473-634-13

```

```

Query Match          15.0%: Score 347; DB 4; Length 348;
Best Local Similarity 28.6%: Pred. No. 9.9e-20;
Matches 99; Conservative 57; Mismatches 132; Indels 58; Gaps 10;

```

```

QY 49 MLLDLTAVAGNAVMVIAKTPALRKRV--FVPHCLVDLALTLMPMLSSALFD 106
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 22 LAVILITVAGNVVCLAVGLNRRLNLTNCFIVSLAITDLLGLVLPF-----SAITYQ 76
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 107 HAL---FGEVACRLYLELSCVFSALISVAINVERIYVYVHMRREVRTGLVASVL 163
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 77 LSCWMSGKVCFCNITSLDVMCLTASILNLFMISLDRCVAMDLRVPVLTTPARVAISL 136
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 164 VGWVVKALAMASVPV-LGRVSWMEGAPS--VPPGCSLQWSHSAVCQLFVYVFAVLFLP 220
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 137 VLIWVISTITLSFLSIHGLMNSRNKTSKGNHTTSKCNQVN-----EYGLVDGLVTFELP 191
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 221 LLLILVYCSMFRAVRAVAAOHGFLPTWMETPRQRSELSRSTMTVSSGAPQTPTRTF 280
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 192 LLIMCITYRIFRVARQAKRIDHSSWK-----AATIREHR-- 228
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 281 GCGKAAYVLLAVGQFLCMLPFPSFHLVYVALSAQPISTGQVESVWIGFCTSPNPF 340
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 229 ---ATVTLAAVMGAFITICMPYFTAFVYRGLRGDDAINEMLEAIVMLGYANSALNPIL 284
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 341 YGCLNROI RGLSKQFCFKPAPEELRLPSREG---SIEENFLQ 383
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 285 YAALNRDFRTGYQQLFCC-----RLANRSHKTSLSRNSAQ 320
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 11
US-08-103-170-4
; Sequence 4, Application US/08103170
; Patent No. 5885824
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Recombinant Genomic Clones Encoding
; TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors. Methods For Production
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/103,170
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/633,060
; FILING DATE: 24-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavallee, Jean-Paul
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-017-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 24885 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0159 US

```

? TELECOMMUNICATION INFORMATION
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
? TELEX:
?
? INFORMATION FOR SEQ ID NO: 5
? SEQUENCE CHARACTERISTICS:
? LENGTH: 359 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: GenBank
? CLONE: 791239
?
US-08-748-485-5

```

Query Match	14.88;	Score 343;	DB 2;	Length 359;
Best Local Similarity	-27.08;	Pred. No. 2.1e-19;		
Matches 99;	Conservative 57;	Mismatches 146;	Indels 64;	Gaps 11;

```

Oy 49 MLLDLTIVAGNAAMAVIAITKTPALRRKVV--FVPHCLCIVDLALTLPMLAMSSSLAFD
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 LIIILIVAGNVVYCVCLAVGLNRRLRLSLTNCFIYSLAVTDLLGLLVPF-----SAITQ 79
Oy 107 HAL--FGEVACRLYLFLSYSCFVSLAISVAISINVERYYYYVHDMRYEVRMTGLVASVL
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 LSCKSFSEKVCNITYTSLDVMICLASILNLEPMISIDRYCAVTDPLRYPVLIITPARVAISL 139
Oy 164 VGWYWKALMAASVPLGLGVNSDEGAPSPVPG-----CSLWMSHAICYQLFVYFAVLITFL 218
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 140 VFIWVITSLTSLFSLI--HLGNNSRNSTSKDNDITVKCKVQYN-----EYGLVDGLVTFY 192
Oy 219 LPLLIILVYVCSMPFVAVVAAHMGRLPTTMEPPRORSESLSRSTVWTSGCAPQTTPHR 278
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 LPLMLCTTTRYIRIFRIAREQARRLNHISMKAA----- 225
Oy 279 TFCGGKAUVVLAVAGGOFLLCMLPEYFSEHLYVALSAOPISIGQVESVVTWIGYFCFTSNP 338
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 TIREHKATVTLAAVWGAATIIICMPYFIYVYRGLGODAVAVEVEDVYMLGYNASMLNP 285
Oy 339 FFYGCGLNQIIGELSKOFVCFCKPAPEEELRP---SHREGSIEENFIQIOTLOGTCPSSESW 395
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 ILIYALNDRDPTAYVHQLFCC-----RLASHNSHETSLIRLNNSQ--LNRSGCQDEPRW 334
Oy 396 -VSRL 400
    : : : : :
Db 335 QEDKPL 340

```

RESULT 14
 US-08-467-568-13
 ; Sequence 13, Application US/08467568
 ; Patent No. 5817477
 ; GENERAL INFORMATION:
 APPLICANT: SOPPET, DANIEL R
 TITLE OF INVENTION: ADENERGIC RECEPTOR
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carella, Byrne, Baln, Giffillan, Cecchi,
 ADDRESSEE: Stewart & Olstein
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: NJ
 COUNTRY: USA
 ZIP: 07068-1739
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,568
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 514

```

: ATTORNEY/AGENT INFORMATION:
:   NAME: Ferraro, Gregory D
:   REGISTRATION NUMBER: 36,134
:   REFERENCE/DOCKET NUMBER: 325800-322
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 201-994-1700
:   TELEFAX: 201-994-1744
:   INFORMATION FOR SEO ID NO: 13:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 359 amino acids
:     TYPE: amino acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:     MOLECULE TYPE: protein
:
: US-08-467-568-13

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Query Match	14.7%;	Score 340;	DB 2;	Length 359;
Best Local Similarity	28.0%;	Pred. No. 3.6e-19;		
Matches 97;	Conservative 57;	Mismatches 134;	Indels 58;	Gaps 9

```

QY 49 MLLDLEPAVAGNAAMVAVIATPALRFV--FVPHCLVDLALATLTPMLAMSSSLFD 106
D 25 LAVILITVAGNVVCLAVGNRLRLNLTNCFIYSLAITDILLGLVLPF-----SAIYQ 79
QY 107 HAL---TGEVACRLYLELSCVFSALILSAINVERTYVYHMRKEVRKTLGLVASVL 163
D 80 LSCWKSQKFCVNCNTYTSIDVNLCASTILNFMISLDRCAAMDRLPVLVTPVPAVSL 139
QY 164 VGWVWKKALAMASVVP-IGRVSMEGAPS--VPQCSIQMSHSAYCQLFVVFAVLYLP 220
D 140 VLIWVISTITSELSIHIGMNSRNETSNGNHTTSCXQVYN-----EYVGLVDGLVTFYLP 194
QY 221 LLLLLVYCSMFRRARVAAMOHGLPTWMETPRORSSELSRSRTMVTSSCAPQTTHRTF 268
D 195 LLIMCITYTRLEKVAROAKRINHIISSMKAA-----T1 227
QY 281 GGGKAAVLLAVGGOFLICMLCPYFSFHLVYALSAQPISTGQVESVYTWIGYCFETSNPF 340
D 228 REHKATVTLAAVMGAFITCMPPYFTAEVYRGDLBGDDAINEVLEAIVLMLGAVANSALNPIL 287
QY 341 YGCLNRQIRGELSQQPVCFFRPAAEEELRLPSRSG---SIEENLQ 383
D 288 YAAUNRDFRTGYQQLFCC-----RLANRSHTKSTLESNSQ 323

```

US-RESULT 15
US-08-748-485-4
Sequence 4, Application US/08748485
Patent No. 5817480
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Goli, Surya K.
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,485
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0159 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 184088
US-08-748-485-4

Query Match 14.7%; Score 340; DB 2; Length 359;
Best Local Similarity 28.0%; Pred. No. 3.6e-19;
Matches 97; Conservative 57; Mismatches 134; Indels 58; Gaps 9;

QY 49 MLLDITAVNGNAVNAVIAKTPALRKY--FVHLCVLDLALTLMLPLMLSSALFD 106
DB 25 LAVLILITVAGNVVCLAVGLNRLRLNCFIVSLAITDLDLGLVLPF----SAIYQ 79
QY 107 HAL--FGEVACRLYLFLSYCFVSLAILSYSAINVERYYVHPMREYEMTLGLVASYL 163
DB 80 LSCKMSFGKVCNIIYSLDVMCTASILNLFMTSLDRYCAVMDPLRYPVLTVPVRAISL 139
QY 164 VGVWVVALAMASYPV-LGRYSWEEGAPS--VPPGCSLQMSHSAICOLEVVFVAVLYFLPL 220
DB 140 VLTIVVISITLSFLSIHLGMSRNETSCKNHTTSKCKVQVN----EYVGLVDGLVTFEYLP 194
QY 221 LLLILVYCSMFRAVVAAMQHGRLPTWMTPRQRSSELSRSTMTSSGAPQTTPHRTF 280
DB 195 LLMCTITTYRIFFVARDQAKRINHISWKAA-----TI 227
QY 281 GGGKAADVLLAVGGQFLICMLPYFSFHLVVALSAOPISITGOVESVYTWIGYFCFTSNPF 340
DB 228 REHKATVTLAAVGAFLICMFYPTAFVYRGLDGDAINEVLAIVMLGYSALNPIL 287
QY 341 YGCLNQIIGELSKQVCFKPAPEEBELRLPSREG---STEENFLQ 383
DB 288 YALNRDFFRTGYOQLFCC-----RLANRNSHKTSLRSNASQ 323

Search completed: December 10, 2002, 09:59:16
Job time : 20 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2002, 09:53:25 : Search time 14 Seconds

(Without alignments)
1336.130 Million cell updates/sec

Title: US-09-838-028-2

Perfect score: 2318
Sequence: 1 MESSPIRQSSGNSSTIGRPV.....SDIIMSDYLPRAPASPRLES 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106	90.9	417	1	GP61_HUMAN
2	823	35.5	428	1	GP61_HUMAN
3	438.5	18.9	368	1	GP61_HUMAN
4	351	15.1	358	1	GP61_HUMAN
5	349.5	15.1	440	1	GP61_HUMAN
6	349	15.1	359	1	GP61_HUMAN
7	345	14.9	358	1	GP61_HUMAN
8	345	14.9	358	1	GP61_HUMAN
9	344	14.8	359	1	GP61_HUMAN
10	343	14.8	359	1	GP61_HUMAN
11	340	14.7	359	1	GP61_HUMAN
12	338.5	14.6	436	1	GP61_HUMAN
13	337	14.5	400	1	GP61_HUMAN
14	335.5	14.5	405	1	GP61_HUMAN
15	335.5	14.5	405	1	GP61_HUMAN
16	335	14.5	428	1	GP61_HUMAN
17	332.5	14.3	572	1	GP61_HUMAN
18	326.5	14.1	400	1	GP61_HUMAN
19	323.5	14.0	405	1	GP61_HUMAN
20	322.5	13.9	418	1	GP61_HUMAN
21	321.5	13.9	398	1	GP61_HUMAN
22	321.5	13.9	405	1	GP61_HUMAN
23	320.5	13.8	562	1	GP61_HUMAN
24	319.5	13.8	408	1	GP61_HUMAN
25	317.5	13.7	379	1	GP61_HUMAN
26	315	13.6	351	1	GP61_HUMAN
27	312.5	13.5	405	1	GP61_HUMAN
28	307	13.2	458	1	GP61_HUMAN
29	306.5	13.2	519	1	GP61_HUMAN
30	305	13.2	515	1	GP61_HUMAN
31	301	13.0	515	1	GP61_HUMAN
32	300.5	13.0	466	1	GP61_HUMAN
33	300	12.9	466	1	GP61_HUMAN

ALIGNMENTS

34	299.5	12.9	539	1	DOP2_DROME
35	298.5	12.9	466	1	ALIA_RABIT
36	295.5	12.7	514	1	ALIA_MOUSE
37	293.5	12.7	478	1	OPNA_HUMAN
38	292	12.6	466	1	ALIA_RAT
39	291.5	12.6	388	1	SH4_HUMAN
40	291	12.6	470	1	ALIA_BOVIN
41	290	12.5	466	1	ALIA_BOVIN
42	289.5	12.5	388	1	SSR4_HUMAN
43	289	12.5	446	1	DADR_MACMU
44	288	12.4	452	1	DADR_BOVIN
45	286.5	12.4	388	1	SH4_CAVPO

RESULT 1	GP61_HUMAN	STANDARD:	PRT:	417 AA.
AC	GP61_HUMAN	GP61_HUMAN		
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Probable G-protein-coupled receptor GPR61 (Biogenic amine receptor-like G-protein-coupled receptor).			
GN	GP61 OR BAUER.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21105913; PubMed=11165367;			
RA	Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M., Lynch K.R., O'Dowd B.F.;			
RT	"Identification of four novel human G protein-coupled receptors expressed in the brain";			
RL	Brain Res. Mol. Brain Res. 86:13-22(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hypothalamus;			
RX	MEDLINE=21548835; PubMed=11690637;			
RA	Cikos S., Gregor P., Koppel J.;			
RT	"Cloning of a novel biogenic amine receptor-like G protein-coupled receptor expressed in human brain";			
RL	Biochim. Biophys. Acta 1521:66-72(2001).			
CC	- FUNCTION: Orphan receptor.			
CC	- TISSUE SPECIFICITY: Expressed in brain; detected in frontal and temporal lobes, occipital pole, amygdala and hippocampus. Also expressed in testis. Low expression in many other tissues.			
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	- CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 415.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF317652; AAK12637.1;			
DR	EMBL; AF258342; AAK97826.1; ALT_FRAME.			
DR	Genew; HGNC:13300; GPR61.			
DR	MIT; 606916;			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPSN.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.			

```
KW G-protein coupled receptor; Transmembrane; glycoprotein.
FT DOMAIN 1 44 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 45 67 1 (POTENTIAL).
FT DOMAIN 68 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 98 2 (POTENTIAL).
FT DOMAIN 99 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 135 3 (POTENTIAL).
FT DOMAIN 136 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 229 5 (POTENTIAL).
FT DOMAIN 230 287 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 288 310 6 (POTENTIAL).
FT DOMAIN 311 324 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 325 344 7 (POTENTIAL).
FT DOMAIN 345 417 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 91 91 L -> P (IN REF. 2).
FT CONFLICT 102 102 P -> S (IN REF. 2).
FT CONFLICT 113 113 V -> M (IN REF. 2).
FT CONFLICT 194 194 H -> G (IN REF. 2).
FT CONFLICT 226 226 L -> V (IN REF. 2).
FT CONFLICT 241 242 PD -> OH (IN REF. 2).
SQ SEQUENCE 417 AA: 45606 MW: 34758041A714F62 CRC64:

Query Match 90.9%; Score 2106; DB 1; Length 417;
Best Local Similarity 98.8%; Pred. No. 1.2e-123;
Matches 409; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MESSPIROSSGNSSTLCRPVOTPEPSTASGVPEGLDVASESVALFEMLLDITAVAGN 60
    |||
DB 1 MESSPIROSSGNSSTLCRPVOTPEPSTASGVPEGLDVASESVALFEMLLDITAVAGN 60
OY 61 AAWAVYAKTPALRKFEVFEHLCLVDLLALTLPRLMLSSALFDHALGECVCRYLF 120
    |||
DB 61 AAWAVYAKTPALRKFEVFEHLCLVDLLALTLPRLMLSSALFDHALGECVCRYLF 120
OY 121 LSVCFVSLATLSVSAINVERYYVYVHPMRREVRMTGLVAVSLGVVWKALAMASVPLG 180
    |||
DB 121 LSVCFVSLATLSVSAINVERYYVYVHPMRREVRMTGLVAVSLGVVWKALAMASVPLG 180
OY 181 RVSMEEGAPVPPGCSLQWMSHAYCOLFVVAVFLPLLLLLVYVYCSMFRARVAAAM 240
    |||
DB 181 RVSMEEGAPVPPGCSLQWMSHAYCOLFVVAVFLPLLLLLVYVYCSMFRARVAAAM 240
OY 241 QHGFLPTWMETPRORSESLSSRSTMTVSSGAPQTPHRTGCGKAAYVLLAVGQFLLCW 300
    |||
DB 241 QHGFLPTWMETPRORSESLSSRSTMTVSSGAPQTPHRTGCGKAAYVLLAVGQFLLCW 300
OY 301 LPYFSEHLVYVALSAQPISTGOVESVVTWIGYFCFTSNPFYGCCLNROI RGLSKQVCFE 360
    |||
DB 301 LPYFSEHLVYVALSAQPISTGOVESVVTWIGYFCFTSNPFYGCCLNROI RGLSKQVCFE 360
OY 361 KPAPPEELRLPSREGSTEENFLQLOGTGCPSSESVRPLSPKQEPADVDFRI 414
    |||
DB 361 KPAPPEELRLPSREGSTEENFLQLOGTGCPSSESVRPLSPKQEPADVDFRI 414

RESULT 2
GPRX_ORVLA
ID GPRX_ORVLA STANDARD: PRT: 428 AA.
AC 091178;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable G-protein-coupled receptor (Fragment).
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=95275927; Pubmed=7756357;
RA Yasuoka A., Abe K., Saigo K., Arai S., Emori Y.;
RT "Molecular cloning of a fish gene encoding a novel seven-transmembrane
RT receptor related distantly to catecholamine, histamine, and serotonin
RT receptors."
RL Blochum. Biophys. Acta 1235:467-469(1995).
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; DA3633; BAA0741.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein.
FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 47 67 1 (POTENTIAL).
FT DOMAIN 68 93 2 (POTENTIAL).
FT TRANSMEM 94 114 2 (POTENTIAL).
FT DOMAIN 115 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 141 3 (POTENTIAL).
FT DOMAIN 142 162 4 (POTENTIAL).
FT TRANSMEM 163 183 5 (POTENTIAL).
FT DOMAIN 184 210 6 (POTENTIAL).
FT TRANSMEM 211 231 7 (POTENTIAL).
FT DOMAIN 232 293 8 (POTENTIAL).
FT TRANSMEM 294 314 9 (POTENTIAL).
FT DOMAIN 315 398 10 (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 428 428
SQ SEQUENCE 428 AA: 47259 MW: 87495875B58A38F CRC64:

Query Match 35.5%; Score 823; DB 1; Length 428;
Best Local Similarity 42.3%; Pred. No. 2.6e-44;
Matches 184; Conservative 81; Mismatches 142; Indels 28; Gaps 11;

OY 2 ESSPI---POSSGNSST--LCRPVOTPEPSTASGVPEGL---RDVASESVALFEMLL 52
    :|||
DB 5 KTSPIITSDHSISNFSGLGEPHFTVP-----PDGVYTSQSOMKDLFGLCFCAVTL 56
OY 53 DLTAVAGNAAMAVYAKTPALRKFEVFEHLCLVDLLALTLPRLMLSSALFDHALGCE 112
    :|||
DB 53 DLTAVAGNAAMAVYAKTPALRKFEVFEHLCLVDLLALTLPRLMLSSALFDHALGCE 112
OY 113 VACRLYFLSVCFVSLATLSVSAINVERYYVYVHPMRREVRMTGLVAVSLGVVWKALA 172
    :|||
DB 113 VACRLYFLSVCFVSLATLSVSAINVERYYVYVHPMRREVRMTGLVAVSLGVVWKALA 172
OY 117 LECOVYIFLWNLFWLILWLSILITAIISVERFYIYVHPMRREVRMTGLVAVSLGVVWKALA 176
    :|||
DB 117 LECOVYIFLWNLFWLILWLSILITAIISVERFYIYVHPMRREVRMTGLVAVSLGVVWKALA 176
OY 173 MASVPVLGRVSMEEGAPVPPGCSLQWMSHAYCOLFVVAVFLPLLLLLVYVYCSMFR 232
    :|||
DB 173 MASVPVLGRVSMEEGAPVPPGCSLQWMSHAYCOLFVVAVFLPLLLLLVYVYCSMFR 232
OY 233 RVARVAAAMOHGP-LPTWMET--PRORSESLSSRSTMTVSSGAPQ-TTPHRTFGCGKAAY 288
    :|||
DB 233 RVARVAAAMOHGP-LPTWMET--PRORSESLSSRSTMTVSSGAPQ-TTPHRTFGCGKAAY 288
OY 297 LAFVCGFLVCLWLPFFTFHLOMSLTGSMKSPGDEAVNMLAVSSFVNPSTYGLNROI 356
    :|||
DB 297 LAFVCGFLVCLWLPFFTFHLOMSLTGSMKSPGDEAVNMLAVSSFVNPSTYGLNROI 356
OY 349 RGLSK-QVCFEKPAPPEELRLPSREGSTEENFLQLOGTGCPSSESVRPLSPK-QE 406
    :|||
DB 349 RGLSK-QVCFEKPAPPEELRLPSREGSTEENFLQLOGTGCPSSESVRPLSPK-QE 406
OY 357 RDELVKFRRCVCTOPV---ETGPSLSEGSFOENFLQRTSSSETHPSFANSNPRNME 413
    :|||
DB 357 RDELVKFRRCVCTOPV---ETGPSLSEGSFOENFLQRTSSSETHPSFANSNPRNME 413
```

QY 407 PPAVDFRIPGIAEE 421
 DB 414 NOA--HKIPGIPPEE 426

RESULT 3

GP62_HUMAN
 ID GP62_HUMAN STANDARD; PRT; 368 AA.
 AC G9B2J7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable G protein-coupled receptor GPR62.
 GN GPR62.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21105913; PubMed=11165367;
 RA Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M.,
 RA Lynch K.R., O'Dowd B.F.;
 RT "Identification of four novel human G protein-coupled receptors
 expressed in the brain.";
 RL Brain Res. Mol. Brain Res. 86:13-22(2001).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in brain; detected in the basal
 CC forebrain, frontal cortex, caudate, putamen, thalamus and
 CC hippocampus.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AF317653; AK12638.1;
 CC Gene: HGNC:13301; GPR62.
 CC MIM: 606917;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 18
 FT TRANSMEM 19 18
 FT TRANSMEM 19 39
 FT DOMAIN 40 53
 FT TRANSMEM 54 74
 FT DOMAIN 75 91
 FT TRANSMEM 92 112
 FT TRANSMEM 113 129
 FT TRANSMEM 130 150
 FT DOMAIN 151 177
 FT TRANSMEM 178 198
 FT DOMAIN 199 239
 FT TRANSMEM 240 260
 FT TRANSMEM 261 272
 FT TRANSMEM 273 293
 FT DOMAIN 294 368
 FT TRANSMEM 294 368
 FT CARBOHYD 3 3
 FT CARBOHYD 8 8
 SO SEQUENCE 368 AA; 37628 MW; 9CFFP95298D12C75 CRC64;

Query Match 18.9%; Score 438.5; DB 1; Length 368;
 Best Local Similarity 31.8%; Pred. No. 1.4e-20;

Matches 127; Conservative 55; Mismatches 146; Indels 71; Gaps 14;

QY 40 ASE---SVALFEMLLDTTAVAGNAAMAVYAKRPAKRFVFRHLCYDIALTLMLPL 96
 DB 9 ASEVAGSLGLTLAAVVEGALLGNGALLVLRTPGLDLYLHLCVDDLLAAASIMPL 68
 QY 97 AMLSSSAL-EDHALGVEACRLYLFLSVCFVSLAALSVAINVERYYVVMREYVMT 155
 DB 69 GLLAAPPGLGRLVLRGAPCAARFLSAAFLPACTIGVAAAGLARYLRIYHPLRGSRPP 128
 QY 156 LGLVASVLGVVKALAMASVPLGRVSWEGADSVPGCSLQMSHAYCOL-----F 208
 DB 129 PVL---VLTAVMAAAGILGALSTL-----GPPAPPPA-----PARCSVLGGLCPF 172
 QY 209 VVFAVLYELLPLLLLVVYCSMFRVARVAMOGPLRTMETPRQSESSSTMTS 268
 DB 173 RPLMALALFALLPLLLLGAVGIFVAVRAALR--PPRA--RGSRLRSDLSRLSTL-- 227
 QY 269 SGAPQTPPHRTFGGKAAYVLLAVGCGFLCMLPYFSFLVYLSAQPISTGOVESVYTW 328
 DB 228 ---PPLRPR--LPGKALALAVGQFACWLY-----GCACLAAPARAADAAVYTW 277
 QY 329 IGYFCFTSNPEFYGCLNRQIR--GELSKQFVCEFFKPAPEBELRLPSREGSIENFLOFL 385
 DB 278 VAYSAPFAHPPFLYGLQRPVRLALGRLSRAL-----PGVPR----- 314
 QY 386 QGTGCPSESWSRPLPSKQEPVADRIIPQIAEEMSE 424
 DB 315 ---ACTPQAMHPRALLCLOLRPFGPAVGPSEAPEQTPPE 350

RESULT 4

ID H2R_RAT STANDARD; PRT; 358 AA.
 AC P25102;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Histamine H2 receptor (H2R) (Gastric receptor I).
 GN H2R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92028890; PubMed=1930188;
 RA Rat M., Traiffort E., Arrang J.-M., Leurs R., Schwartz J.-C.;
 RT "Cloning and tissue expression of a rat histamine H2-receptor gene";
 RL Biochem. Biophys. Res. Commun. 179:1470-1478(1991).
 CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
 CC ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 CC PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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```

FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 44 1 (POTENTIAL).
FT DOMAIN 45 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 81 2 (POTENTIAL).
FT DOMAIN 82 92 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 93 114 3 (POTENTIAL).
FT DOMAIN 115 134 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 135 159 4 (POTENTIAL).
FT DOMAIN 160 179 5 (POTENTIAL).
FT TRANSMEM 180 203 6 (POTENTIAL).
FT DOMAIN 204 233 6 (POTENTIAL).
FT TRANSMEM 234 257 6 (POTENTIAL).
FT DOMAIN 258 266 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 267 288 7 (POTENTIAL).
FT DOMAIN 289 358 7 (POTENTIAL).
FT SITE 98 98 ESSENTIAL FOR HISTAMINE BINDING (BY SIMILARITY).
FT SITE 185 185 ESSENTIAL FOR HISTAMINE BINDING (BY SIMILARITY).
FT SITE 189 189 ESSENTIAL FOR TIOTIDINE BINDING AND IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
FT SITE 189 189 IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 91 173 BY SIMILARITY.
SO SEQUENCE 358 AA; 40253 MW; 4889F69B7B5D5DC CRC64;

```

Query Match 15.1%; Score 351; DB 1; Length 358;
Best local similarity 27.5%; Pred. No. 3.5e-15;

Matches 106; Conservative 58; Mismatches 150; Indels 72; Gaps 12;

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QY 43 SVALFEMLLDLTAVAGNAVAVIAKTPALRKFV--EFHCLVDLLAALTPLAMLS 100
DB 22 SVLTLLTLLI--TLAGNVVVCVAVSLNRRLSLTNCFTVSLATDILLGLVLPF---- 74
QY 101 SSALFPHAL--FGEVACRLYFLSCFVSLATLSVSAIVRYVYVHPMRREVMTLS 157
DB 75 -SAIYOLSTWMSGHVFCNTYITSLDWLCTASLLNLFMSLDKRCVATDPLRIPVLTPY 133
QY 158 LVASLVGVVWVVALAMASVPLGRVSMEE-----GAPSVPGCSLQWMSHAYCOLFVVV 211
DB 134 RVAISLVFLVWISITLSFLSI--HLCWNSRNGTRGNDPFC--CKQYVN-----EYGLV 184
QY 212 FAVLYLPLLLLLLVYVCSMFERRVAAOHGLPTMMEPRRORSESLSRSTMTVSSGA 271
DB 185 DGLVTFYLLPLLMCVYIRFKIARQAKRINISSWKA----- 224
QY 272 PQTTPHRTFGGKAAYVLLAVGQFLCMLPRSFHLYVALSAQPISTGQVESVMTWIGY 331
DB 225 -----TIREKATVTLAAYVGAFTICMFPTTAFYRGLRGDDALINEAVEGIVMLG 277
QY 332 FCFSTNPFFYGCINQIRGELSKQVCFKRP--APEEELRL-----PSREGSIEENF 381
DB 278 ANSALNPILYALNDRFRAVYQDLPHCKFASHNSHKTSLRLNNSLPRGSRGRNQEEK 337
QY 382 LQFLGTCGPSESWSRPLPSKQEP 407
DB 338 PLKIQ-----VMSGTELLHPQGNP 356

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RESULT 5

5H6_HUMAN STANDARD; PRT; 440 AA.

```

AC P50406; Q13640;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE 5-Hydroxytryptamine 6 receptor (5-HT-6) (Serotonin receptor).
GN HTR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC TISSUE-Striatum;
RX MEDLINE=96102917; PubMed=8522988;
RA Cohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
RA Sibley D.R., Roth B., Handlin M.W.;
RT Cloning, characterization, and chromosomal localization of a human
RT 5-HT6 serotonin receptor.;
RL J. Neurochem. 66:47-56(1996).
RN [2]
RP SEQUENCE OF 215-280 FROM N.A.
RC TISSUE-Striatum;
RX MEDLINE=95385798; PubMed=7656980;
RA Ullmer C., Schumack K., Kalkman H.O., Lubbert H.;
RT Expression of serotonin receptor mRNAs in blood vessels.;
RL FEBS Lett. 370:215-221(1995).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
CC 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTROPHIC AGENT, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATE ADENYLATE
CC CYCLASE. IT HAS A HIGH AFFINITY FOR TRICICLIC PSYCHOTROPIC DRUGS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SEVERAL HUMAN BRAIN REGIONS. MOST
CC PROMINENTLY IN THE CAUDATE NUCLEUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L41147; AAA92622.1; -
DR EMBL: Z49119; CAAB8929.1; -
DR Genew; HGNC:5301; HTR6.
DR MIM: 601109; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1.
DR PROSITE: PS00237; G_PROTEIN_REC_P1.1;
DR PROSITE: PS00262; G_PROTEIN_REC_P1.2;
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 166 4 (POTENTIAL).
FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 208 5 (POTENTIAL).
FT DOMAIN 209 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 290 6 (POTENTIAL).
FT DOMAIN 291 295 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 296 320 7 (POTENTIAL).
FT DOMAIN 321 440 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 180 BY SIMILARITY.
FT CONFLICT 247 247 V -> M (in ref. 2).
SO SEQUENCE 440 AA; 46954 MW; C888F47650C1D2EF CRC64;

```

Query Match 15.1%; Score 349.5; DB 1; Length 440;

Best local similarity 30.7%; Pred. No. 5.2e-15; Matches 127; Conservative 59; Mismatches 171; Indels 57; Gaps 18;

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QY 19 VQTPGPSTAGVPEVGLDVASES---VALFEMLLDLTAVAGNAVAVIAKTPALR 74
DB 2 VPE-PGP-TANSTPAGWAGPAPSGSGWVAALCVIALTA-AANSLITALICQPALR 58
QY 75 KF--VFVHCLVDLLAALTPLAMLSVALFEDHAEVAVCRILYFLFVGVSLATLS 132
DB 59 NTSNFFVSLFTSDLMVAVGVMPAPL--NALYGRVVALRGCLLMTADVACCSASILN 116

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RP SEQUENCE FROM N.A.
 RC STRAIN-129/Ola; Pubmed-8938453;
 RX MEDLINE-97092891; Kojayeshi T., Inoue I., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Watanabe T.;
 RT "Cloning, RNA expression, and chromosomal location of a mouse
 RL histamine H2 receptor gene."
 RL Genomics 37:390-394(1996).
 CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
 CC ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 CC PROTEIN WHICH ACTIVATES ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: D50096; BAA08792.1; -
 CC MGI: 108482; Hrh2.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsin.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_FL2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 22
 FT TRANSMEM 23 44
 FT DOMAIN 45 57
 FT TRANSMEM 58 81
 FT DOMAIN 82 92
 FT TRANSMEM 93 114
 FT DOMAIN 115 134
 FT TRANSMEM 135 159
 FT DOMAIN 160 179
 FT TRANSMEM 180 203
 FT DOMAIN 204 233
 FT TRANSMEM 234 257
 FT DOMAIN 258 266
 FT TRANSMEM 267 288
 FT DOMAIN 289 358
 FT SITE 98 98
 FT SITE 185 185
 FT SITE 185 185
 FT SITE 189 189
 FT SITE 189 189
 FT CARBOHYD 4 4
 FT DISULFID 91 173
 FT DISULFID 173 40379 MW; D3DBA81D71B6D927 CRC64;
 SQ SEQUENCE
 Query Match 14.9%; Score 345; DB 1; Length 358;
 Best local Similarity 27.6%; Pred. No. 8.2e-15;
 Matches 108; Conservative 58; Mismatches 152; Indels 74; Gaps 12;

Db 179 EVGLVDGNTVTFYLLIMCVTYRIKRIAREQAKRINHISMWAA----- 224
 Qy 266 VTSSGAPQTPHRRFGGKAAVYLLAAGGFLCWLTFPSFHLVALSADPISIGQYESV 325
 Db 225 -----TIRHKATVTLLAAVMAFYCMFIFYFRTGRLGDDPVNEVEGI 271
 Qy 326 VTWIGYFCFTSNPFYGCILNRQIRGELSOKFVCFK--APPEELRL-----PSREG 375
 Db 272 VLMGIVANSALNPILTYLTNRDPRMAVQQLFHCFLASHNSHKTSRLRNLSLSQSGREG 331
 Qy 376 SIEENFLQIQTGTCPSSESVSRPLSPKQEP 407
 Db 332 RWDEKPLKIQ-----VWSGTELRHQCSP 356
 RESULT 8
 ALAD-RABIT STANDARD; PRT; 576 AA.
 ID ALAD-RABIT
 AC 002666;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 GN Alpha-1D adrenoergic receptor (Alpha 1D-adrenoceptor).
 OS ADRA1D.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI-TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-97182161; Pubmed-9030207;
 RA Suzuki F., Miyamoto S., Takita M., Oshita M., Watanabe Y.,
 RA Kakizuka A., Narumoto S., Taniguchi T., Muramatsu I.;
 RT "Cloning, functional expression and tissue distribution of rabbit
 RL alpha 1d-adrenoceptor."
 RL Biochem. Biophys. Acta 1323:6-11(1997).
 CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
 CC THROUGH THE INFLUX OF EXTRACELLULAR CALCIUM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: U64032; AAB53098.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsin.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_FL2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 101
 FT TRANSMEM 102 126
 FT DOMAIN 127 138
 FT TRANSMEM 139 164
 FT DOMAIN 165 174
 FT TRANSMEM 175 197
 FT DOMAIN 198 218
 FT TRANSMEM 219 243
 FT DOMAIN 244 256
 FT TRANSMEM 257 280
 FT DOMAIN 281 353
 FT TRANSMEM 354 378
 FT DOMAIN 379 385
 FT TRANSMEM 386 410
 FT TRANSMEM 410 410

DB 327 RDEKRALGRVPCVHCP-PEHRASPSMTSHSGARPLSLQOVLPLPLPPNSDSDA 385
QY 376 STENETLOFLOGTGCPSSESVSRPLSPKQEPAYDRIHQIAAE 421
DB 386 SGGTSGLOLTAQLLPLPEA--TRDPPPTATPVTYVNEFTDSVEPE 429

RESULT 10
HHR2_CAVPO STANDARD: PRT: 359 AA.
ID HHR2_CAVPO
AC P47747;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histamine H2 receptor (H2R) (Gastric receptor 1).
GN HHR2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Strain-Hartley; TISSUE-Liver;
RA Traillfort E.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
PROTEIN WHICH ACTIVATE ADENYLYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL: U25440; AAA65713.1; -
DR HSSP: P29274; 1MH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 22
FT TRANSMEM 23 44
FT DOMAIN 45 57
FT TRANSMEM 58 81
FT DOMAIN 82 92
FT TRANSMEM 93 114
FT DOMAIN 115 134
FT TRANSMEM 135 159
FT DOMAIN 160 180
FT TRANSMEM 181 204
FT DOMAIN 205 234
FT TRANSMEM 235 258
FT DOMAIN 259 267
FT TRANSMEM 268 289
FT DOMAIN 290 359
FT SITE 98
FT SITE 186
FT SITE 190
FT SITE 190
FT CARBOHYD 4 4
FT DISULFID 91 174
SQ SEQUENCE 359 AA: 40556 MW: 58DB81BD8FC3C0E9 CRC64;

Query Match 14.8%; Score 343; DB 1; Length 359;
Best Local Similarity 27.0%; Pred. No. 1, 1e-14;
Matches 99; Conservative 57; Mismatches 146; Indels 64; Gaps 11;
QY 49 MLLDLITAVAGNAVMAVIAKTPALRKFFV--FVFHCLVDLALATLMLPLMLSSALFD 106
DB 25 LITLITVTVAGNVVCLAVGLNRRRLSTNCFTVSLAVTDLGLLVLP-----SAIVQ 79
QY 107 HAL---FGEVACRLYLFLSCFVSALTSANVERYYVPMREVMATGLVASV 163
DB 80 LSCWSEFSKVECNITVSLDVMCTASTLNFMTSLDRYCAVTPDLRPVLTIPARAISL 139
QY 164 VGVWVKALMAASVPVLCGRVMEGAPSVPG-----CSLQMSHAYCOLVVFVAVLYFL 218
DB 140 VFLWVISTITSLFSLI--HLCMSNRNRSKNDPIYCKQVYN-----EYGLVDGLVTFY 192
QY 219 LPLLILVYCSMFVRVARVAMQHGPIVWETPRORESLSRSRTVYSSGAPQTTPHR 278
DB 193 LPLLIMCTVFYFIKIAREQARRINHGSKAA----- 225
QY 279 TFGGKAANVLLAVGGFLLCMLPYFSFHLVYALSAQISTGVESVYTWIGYCFITSNP 338
DB 226 TIREHKAATVTLAAVMGAFIICWPFYTFVYRGILKGDADVAVNEFEDVYVLMGLANSALNP 285
QY 339 FFYGCINROIRGELSKQFVCFPPAPEEELRLP---SREGSIEENFLOFLOGTGCPSSEW 395
DB 286 ILVAALNRDRTAYHQIFCC-----RLASHNSHERSLNLNNSQ-LNRSQCQEPHW 334
QY 396 -VSRL 400
DB 335 QEDKPL 340

RESULT 11
HHR2_HUMAN STANDARD: PRT: 359 AA.
ID HHR2_HUMAN
AC P25021; Q1464;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Histamine H2 receptor (H2R) (Gastric receptor 1).
GN HHR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91337087; PubMed=1714721;
RA Gantz I., Munzert G., Tashiro T., Schaeffer M., Wang L.-D.,
RA DelValle J., Yamada T.;
RT "Molecular cloning of the human histamine H2 receptor";
RL Biochem. Biophys. Res. Commun. 178:1386-1392(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Liver;
RX MEDLINE=95275318; PubMed=7755641;
RA Nishi T., Koike T., Oka T., Maeda M., Futai M.;
RT "Identification of the promoter region of the human histamine H2-
RT receptor gene";
RL Biochem. Biophys. Res. Commun. 210:616-623(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99297624; PubMed=10371214;
RA Murakami H., Sun-Wada G., Matsumoto M., Nishi T., Wada Y., Futai M.;
RT "Human histamine H2 receptor gene: multiple transcription initiation
RT and tissue-specific expression1.";
RL FEBS Lett. 451:327-331(1999).
RN [4]
RP SEQUENCE OF 4-351 FROM N.A., AND POLYMORPHISM.
RC TISSUE-Brain;
RX MEDLINE=96414531; PubMed=8817552;

RA	Orange P.R., Heath P.R., Wright S.R., Pearson R.C.A.:
RT	"Allelic variations of the human histamine H2 receptor gene."
RL	NeuroReport 7:1293-1296(1996).
RN	[5]
RP	REVIEW.
RX	MEDLINE=98042107; PubMed=9374694;
RA	Delvalle J., Gantz I.:
RT	"Novel insights into histamine H2 receptor biology.";
RL	Am. J. Physiol. 273:G987-G996(1997).
CC	-1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC ACID SECRETION. ALSO APPEARS TO REGULATE GASTROINTESTINAL MOTILITY AND INTESTINAL SECRETION. POSSIBLE ROLE IN REGULATING CELL GROWTH AND DIFFERENTIATION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE AND, THROUGH A SEPARATE G PROTEIN-DEPENDENT MECHANISM, THE PHOSPHOINOSITIDE/PROTEIN KINASE (PKC) SIGNALING PATHWAY (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- MISCELLANEOUS: ANTAGONISTS FOR THIS RECEPTOR HAVE PROVEN TO BE EFFECTIVE THERAPY FOR ACID PEPTIC DISORDERS OF THE GASTROINTESTINAL TRACT. CERTAIN ANTAGONISTS ARE USED IN THE TREATMENT OF NEUROPSYCHIATRIC AND NEUROLOGICAL DISEASES SUCH AS SCHIZOPHRENIA, ALZHEIMER'S DISEASE AND PARKINSON'S DISEASE.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
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CC	-----
DR	EMBL; M64799; AAA58647.1; .
DR	EMBL; D49783; BAA08618.1; .
DR	EMBL; AB023486; BAA84279.1; .
DR	EMBL; X98133; CAA66832.1; .
DR	PIR; JH0449; JH0449.
DR	HSSP; F29274; IMMH.
DR	Genew; HGNC:5183; HRH2.
DR	MIM; 142703;
DR	InterPro: IPR000276; GPCR_Rhodpsn.
DR	Pfam: PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; G_PRRHODOPS.
DR	PROSITE; PS00237; G_PROTEIN_RECEP.F1.1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECEP.F1.2; 1.
KM	G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT	DOMAIN 1 22
FT	TRANSMEM 23 44
FT	DOMAIN 45 57
FT	TRANSMEM 58 81
FT	DOMAIN 82 92
FT	TRANSMEM 93 114
FT	DOMAIN 115 134
FT	TRANSMEM 135 159
FT	DOMAIN 160 180
FT	TRANSMEM 181 204
FT	DOMAIN 205 234
FT	TRANSMEM 235 258
FT	DOMAIN 259 267
FT	TRANSMEM 268 289
FT	DOMAIN 290 359
FT	SITE 98 98
FT	SITE 186 186
FT	SITE 190 190
FT	CARBOHYD 4 4
FT	DISULFID 91 174
FT	VARIANT 217 217
FT	N->D.
FT	/FTID=VAR_000958.
FT	K->R.

FT				/FTID=VAR_009959.
FT	VARIANT	268	268	V -> M.
FT				/FTID=VAR_009960.
FT	CONFLICT	133	133	V -> A (IN REF. 4).
FT	CONFLICT	175	175	K -> N (IN REF. 4).
FT	CONFLICT	207	207	K -> R (IN REF. 4).
SO	SEQUENCE	359 AA:	40098 MW;	9835AE2BA60B9B0F CRC64:
Query Match		14.7%;	Score 340;	DB 1; Length 359;
Best Local Similarity		28.0%;	Pred. No. 1.7e-14;	
Matches 97;		Conservative 57;	Mismatches 134;	Indels 58; Gaps 9
OY	49	MILLDLTVAGAAVMAVIATKTPALRKVE--FEVHLCTVDLLAALTPLMLAMISSSLAFD	106	
Dd	25	LAVLITLVAGNVVCLAVGLNRRLNRLNCRIVSAIADLDLGLVLDPF-----SAIQO	79	
OY	107	HALL---FGEVACRLTFLTSVCFSVALISVSAINERYVVVPHMRKYEVRMTLGVAASVL	163	
Dd	80	LSCKMSFGVPCNTITSLDVMICTASILNEMISLDRCAYMDPLPVLVTPVRAAISL	139	
OY	164	VGWVKALAMASVPY-LGRHWSMEGAPS--VPPGCSLQMSHSAYCOLFEVVFPAVLFFLP	220	
Dd	140	VLIVWISITSLPSLIHLGNMNSRNEJSSKGHTSKCQVQN-----EYGLVDGLVTFYLP	194	
OY	221	LLLLIVVYCSMFVARVAAMOHGPLPTWMETPRORSELSNSTVYTSSGAPOTTPHRTE	280	
Dd	195	LLIMCIITYRIKFVARDOAKRHNIHSSMKAA-----TI	227	
OY	281	GCGKAAYVLLANGGOFLICWLPEFSFHLYVALSAOPISNGOVESVTWIGPCFTSNPF	340	
Dd	228	REHKRTVTTLAAWGAFTICMPFYTAIFYRGLDDAINEVLEATVLMGIYANSALNPILL	287	
OY	341	YGCLRQIRGELSQQVCFEPKPAEBELRLPSREG---SIENEFLO	383	
Dd	288	YAALNRDRFRTGYQLFCF-----RLANRNSHKTSLRNSAQ	323	
RESULT 12	5H6_RAT			
ID	5H6_RAT	STANDARD;	PRT;	436 AA.
AC	P31388;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	5-Hydroxytryptamine 6 receptor (5-HT ₆) (Serotonin receptor)			
DE	(SM-B17).			
CN	HR6.			
OS	Rattus norvegicus (rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCHI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Striatum;			
RX	MEDLINE=93196608; PubMed=7680751;			
RA	Monsma F.J., Jr., Shen Y., Ward R.P., Hamblin M.W., Sibley D.R.;			
RT	"Cloning and expression of a novel serotonin receptor with high			
RT	affinity for triacyclic psychotropic drugs.";			
RL	Mol. Pharmacol. 43:320-327(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=93227562; PubMed=8389146;			
RA	Ruat M., Traifort E., Arrang J.-M., Tardivel-Lacombe J., Diaz J.,			
RA	Leurs R., Schwartz J.-C.;			
RT	"A novel rat serotonin (5-HT ₆) receptor: molecular cloning,			
RT	localization and stimulation of cAMP accumulation.";			
RL	Biochem. Biophys. Res. Commun. 193:268-276(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	Strain=Wistar;			
RA	Maternal R.;			
RL	Submitted (xxx-1993) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR			

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CC      5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC      AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC      THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATE ADENYLATE
CC      CYCLASE. IT HAS A HIGH AFFINITY FOR TRICICLIC PSYCHOTROPIC DRUGS.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: LOCALIZED EXCLUSIVELY IN THE CENTRAL NERVOUS
CC      SYSTEM, PREDOMINANTLY IN THE CORPUS STRIATUM BUT ALSO IN VARIOUS
CC      LIMBIC AND CORTICAL REGIONS.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; L03202; AAA40618.1; -
CC      EMBL; S62043; AAB26908.1; -
CC      EMBL; L19656; AAA40611.1; -
CC      InterPro: IPR000276; GPCR_Rhodopsn.
CC      Pfam: PF00001; 7tm.1; 1
CC      PRINTS; PR00237; GPCRHOPOPSN.
CC      DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC      DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC      KM G-protein coupled receptor; Transmembrane; Glycoprotein;
CC      Multigene family.
CC      FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 35 57 1 (POTENTIAL).
CC      FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 65 85 2 (POTENTIAL).
CC      FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 101 122 3 (POTENTIAL).
CC      FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 145 166 4 (POTENTIAL).
CC      FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 185 208 5 (POTENTIAL).
CC      FT DOMAIN 209 265 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 266 290 6 (POTENTIAL).
CC      FT DOMAIN 291 295 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 296 320 7 (POTENTIAL).
CC      FT DOMAIN 321 436 7 (POTENTIAL).
CC      FT CARBOHYD 9 9 CYTOPLASMIC (POTENTIAL).
CC      FT DISULFID 99 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      FT CONFLICT 57 57 L -> V (IN REF. 1).
CC      FT CONFLICT 336 436 PCVCPPEHRPALPPPPCPPLTAVPPOASACSRCLICRO
CC      TQIQTPGAPRRACSSQSPFCCLERPPGPRHPRPLUNST
CC      SLSQTLMSLRGRHISVPP -> HASTVPSSTQPCPLPHV
CC      DLSQRCQTRQLOQVIALPLPNSDSASGSGTSGQLTAQ
CC      LLLPGCATRPPPPTRATTVVNFVDVSEPEIRPHPLSP
CC      VN (IN REF. 1).
CC      SO SEQUENCE 436 AA; 46922 MW; 6BC00F6A3CBA5B4 CRC64;
Query Match 14.6%; Score 338.5; DB 1; Length 436;
Best Local Similarity 28.4%; Pred. No. 2,5e-14;
Matches 129; Conservative 58; Mismatches 171; Indels 97; Gaps 20;
OY 2 ESSPIPOSSSSSLGVPTQPGSTASGVPEGLRDVASVSAFPMFLDLTLAVAGNA 61
DB 4 EPGPV-----NSST---PAMGPPPPAPG-----GSGWVAALCVIIVLTA-AANS 45
OY 62 AVNAVIATKPAALRRK--VEVFHCLVDLALTLPLMLSSSLAFDHALGFEVACRLYL 119
DB 46 LLLVLCIQALANTSNFLVLSFTSDLMVGLVVMPPML-NALVGRWVLANGLCILMT 103
OY 120 FLVSCVSLAIVSAIINVERIYVVPMPREYKMTGLVASLVGVWVAKALMASYPVL 179
DB 104 AFDVMCCSASILCLISLDRIYLSPLRYKRLMTAPRALALILGAMSLAALAFPLL 163
OY 180 GRYSWE-CAPSPV-PCGSLQMSHSAVCOL-----PVVAVAVLYELLPLLLIVVCSMF 232
DB 164 --LGWHELGAARTAPAG-----QCRLLASLPFVLVASGVTFPLPSGALIGFTYCRIL 212

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OY 233 RVARVAAMOGPLEPTWM-----ETPRORESLSSRSTWTSAGAPQTPHRTFG 281
DB 213 LAARKQAVQVASLTTGAGALLETLOYPRTPRGMESADSRRLATKIRKAL----- 264
OY 282 GKRAAVLLAVGQFLCMLPYFSFHLVALSAQISTGVESVYTWIGFCTSNPFY 341
DB 265 --KASLTGLIGLMFEVWTMLPFVANIQAQV-CDICISPLFD-VLTWLGVCNSTMNPILY 320
OY 342 GCUNROIRGSLSKQFVCFEFPAPPEELRP-----SREGSI 377
DB 321 PLPMRDFKRALGRPLCVHCP-PEHRPALPPPCGILTAVPDASACSRCLCLCROTQI 379
OY 378 EENFLQIGT--GC--PSESWSRPLSPKQEP 407
DB 380 QTP---LOGAPRACSSQSPFCCLERPPGPRHPR 410
RESULT 13
B3AR_RAT
ID B3AR_RAT STANDARD: PRT: 400 AA.
AC P26255;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Beta-3 adrenergic receptor.
GN ADRB3 OR ADRB3R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
ON [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084710; PubMed=1721063;
RA Muzzin P., Revelle J.P., Kuhne F., Gocayne J.D., McCombie W.R.,
RA Venter J.C., Giacobino J.-P., Fraser C.M.;
RT "An adipose tissue-specific beta-adrenergic receptor. Molecular
RT cloning and down-regulation in obesity.";
RL J. Biol. Chem. 266:24053-24058(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92100057; PubMed=1684635;
RA Granneman J.G., Lahners K.N., Chaudhry A.;
RT "Molecular cloning and expression of the rat beta 3-adrenergic
RT receptor.";
RL Mol. Pharmacol. 40:895-899(1991).
RP [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93178631; PubMed=8382630;
RA Bensaid M., Kaghad M., Rodriguez M., Le Fur G., Caput D.;
RT "The rat beta 3-adrenergic receptor gene contains an Intron.";
RL FEBS Lett. 318:223-226(1993).
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
CC THERMOGENESIS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES, AND DIGESTIVE
CC TRACT.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; M74716; AAA74470.1; -
CC      EMBL; S73473; AAB20702.1; -
CC      EMBL; S56481; AAB25520.1; -
CC      EMBL; S56152; AAB25521.1; -

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FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 178 4 (POTENTIAL).
FT DOMAIN 179 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 225 5 (POTENTIAL).
FT DOMAIN 226 292 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 293 314 6 (POTENTIAL).
FT DOMAIN 315 326 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 327 347 7 (POTENTIAL).
FT DOMAIN 348 405 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 189 BY SIMILARITY.
FT LIPID 361 361 PALMITATE (BY SIMILARITY).
FT CONFLICT 6 7 A -> T (IN REF. 4).
FT CONFLICT 156 156 P -> HE (IN REF. 3).
SQ SEQUENCE 405 AA: 42903 MW: C93667DC1CC286F8 CRC64:

Query Match 14.5%: Score 335.5; DB 1; Length 405;
Best Local Similarity 28.1%: Pred. No. 3.5e-14;
Matches 121; Conservative 67; Mismatches 183; Indels 59; Gaps 18;

QY 7 POSSGNSSTGRVQRP--GPST--ASGVEVGLRDVASESVLFFMLLLDLTVAGNAA 62
DB 3 PWRPGNS-LTPMDIPTLTAPNTANASGLPGVPW---AAVLAGALLAVLATVGNLL 57
QY 63 VMAVIKTPALRRF--VFVHCLVDLLAALTMLPLAMSSALFDHALFGEVACRLYLF 120
DB 58 VIVAIAATPRLQMTNVEFVSLATADLVGLLVVPG--ATLALTGHWPLGVTGCELMTS 115
QY 121 LSCFVSLALISVAIVERIYVHPRYEVRMTGLVASVLYGVVAKALANASVVLG 180
DB 116 VDVLCTVASTETLCALAVDYLATNPLRGALTKRRALAAVLLVWVSAVSEFAPIMS 175
QY 181 RVSMEEGAPVPPGCSLQMSHSAVCOL-----FVVVFAVLYFLPLLLITLVCSMPRVA 235
DB 176 K-WMRIGADAEQRCH---SNPRCCTFASMPALLSSSYFLPLVLMFVARVVA 231
QY 236 ----RVAAMQHPLTWEMTPR-ORSESLSSRSTWTSNGAP-----OTPHRTFGGG 283
DB 232 TROLRLRLRRLGFRPEESPAPASRSGSPGLAGCAPACVPSYGRPARLLPLREH--- 288
QY 284 KAAVLLAVGCGFLCMLPFPSFHLVYALSAQPISTQOVESVYTWIGFETSPFFYGC 343
DB 289 RAIRRTGLLNGTFTLCLPFFVNVVVALGSPSLVGPFLALMWLDVANAANFPLLY-C 347
QY 344 LNRQIGELSKQFCFKPAPPEELRL--PSREGISENLFQLOGCPSESVNSPRLP 401
DB 348 RSPDFRRAF-RRLLC--RCRPEELAAASPPR-----APSGAPTALTSP 388
QY 402 SPKQEPRAVD 411
DB 389 AGPMQPELD 398

RESULT 15
ALAD-RAT STANDARD; PRT; 561 AA.
AC P23944;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
adrenergic receptor) (RA42).
GN ADRA1D OR ADRA1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=91177869; PubMed=1706716;
RA Lomansney J.W., Cotechia S., Lorenz W., Leung W.-Y., Schwinn D.A.,

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RA Yang-Feng T.L., Brownstein M., Lefkowitz R.J., Caron M.G.;
RT "Molecular cloning and expression of the cDNA for the alpha 1A-
RT adrenergic receptor. The gene for which is located on human
RT chromosome 5."
RL J. Biol. Chem. 266:6365-6369(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95114877; PubMed=7815325;
RA Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA Norman N.P., Campbell S., Fidock M.D., Furness L.M.,
RA Parry-Smith D.J., Peter B., Bailey D.S.;
RT "Cloning and pharmacological characterization of human alpha-1
RT adrenergic receptors: sequence corrections and direct comparison with
RT other species homologues."
RJ J. Pharmacol. Exp. Ther. 272:134-142(1995).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
CC THROUGH THE INFLUX OF EXTRACELLULAR CALCIUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: VAS DEFERENS, HIPPOCAMPUS, CEREBRAL CORTEX,
CC AORTA, BRAIN STEM, HEART AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: M60654; AAA63477.1; -.
DR EMBL: L31771; AAB59704.1; -.
DR PIR: A38731; A38731.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 90
FT TRANSMEM 91 115
FT DOMAIN 116 127
FT TRANSMEM 128 153
FT DOMAIN 154 163
FT TRANSMEM 164 186
FT DOMAIN 187 207
FT TRANSMEM 208 232
FT DOMAIN 233 245
FT TRANSMEM 246 269
FT DOMAIN 270 342
FT TRANSMEM 343 367
FT DOMAIN 368 374
FT TRANSMEM 375 399
FT DOMAIN 400 561
FT CARBOHYD 60 60
FT CARBOHYD 76 76
FT LIPID 413 413
FT DOMAIN 21 57
FT CONFLICT 416 421
FT CONFLICT 424 483
SQ SEQUENCE 561 AA: 59354 MW: B6537DCAD47BE2 CRC64:

Query Match 14.5%: Score 335.5; DB 1; Length 561;
Best Local Similarity 25.7%: Pred. No. 4.8e-14;
Matches 125; Conservative 81; Mismatches 195; Indels 85; Gaps 19;

QY 6 IPOSSGNSSTLGR-----VPOTPGPSTASGVEVGLRDVASESVLFFMLLLD 53
DB 42 VPGATGGAVVGTGGSGEDNOSTGEPGAASGEVNSAAVGLVVAQGVGVFLAFT 101

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Oy	54	LEAAVANAAMAAVIAKPPALPKFV--FVPHCLITVDLLAALTIMPLAMSSALFDHALRG	111
Dd	102	LTAAGNLVLTVLVAACNRHLOTNTNFTVNLDAVADLLSAALPFS--ATMEVLGFMAEG	159
Oy	112	EVACRLVLELTVCSFVSALISVSAINERYYYVYVHPARYEVRMTGLGVASVLGVVAKAL	171
Dd	160	RTFCDDVMAAVDVLCTASILSLCTISYDVRGVHSLKPAIMTERKAAAILMLMAVNL	219
Oy	172	AMASVPVLGRVSWEGARVSVPGCSLOMSHAYQL-----FVYVFAVLFLLPLLLILY	226
Dd	220	VVSVPFLG---MKE---PVPP-----DERFCGIIEGVYAIFFSVCSFYLPMAYIV	266
Oy	227	VYCSMFYAR--VAAOHGRLPTMNETPRDSE---SLSSRTMVSSGAP--QTAPHRT	279
Dd	267	MYCRVYVVARSTTSLSENG-----IKREPKASEVYLIRHCGAITSKAGYIPQSSKGHT	322
Oy	280	FGGG-----KAAVVLAVGGQFLICMLPYFSFHLVYALSAPISTGOVESVYV	327
Dd	323	LRSLSVLRLLFKFSREKKAALKLAIYGVFVLCWPFPEFVPLSLSPQLKPSGVEKVI	382
Oy	328	WIGYFCFTSNPFYFGCJNRQIRGSLSKQFOCFMPPAPEEELRLPSRGSTEENFDFLG	387
Dd	363	WLGTFNSCVNLLIYPCSSRE-----FKRALRLRLKQCCR--RRRLMAVIG	427
Oy	388	TGCPSESVWVSR--LPSKDEPPAVDERI---PQIAEETSEFLQDITSDIIMSDSYLR	442
Dd	428	HHMRASTDARSDCAPSPRIAPCAPRLALVLAHPGASADPPE-----TQDVSSSR--K	479
Oy	443	PAASPR	448
Dd	480	PASALR	485

Search completed: December 10, 2002, 09:57:42
Job time : 17 secs

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